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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 10, 2005, 11:21:18 : Search time 3299 Seconds  
(without alignments)

1662.808 Million cell updates/sec

Title: US-10-659-782A-32

Perfect score: 616

Sequence: 1 MPSPGTVCSULLLGMWLSDL.....PPSSRERSRRSHQPSCSPEL 116

Scoring table: BL05062

Xgapext 10.0 Xgapext 0.5  
Ygapext 10.0 Ygapext 0.5  
Fgapext 6.0 Fgapext 7.0  
Delop 6.0 Delext 7.0

Searched: 4526729 seqs., 23644849745 residues

Total number of hits satisfying chosen parameters: 90534458

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Command line parameters:

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-MODEL:frame+ p2n.model -DEV=xlh
-O:/cgn2.1/USPTO_spool/US10659782/runat_05022005_161917_4270/app_query.fasta_1.263
-DB:GenEmb1 -QFM=fascap -SUFFIX=rge -MINNATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX:blossom62 -TRANS=human40_cdi -LIST=5
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US10659782 @CGN 1-3731 @runat 05022005_161917_4270 -NCPU=6 -ICPU=3
-NO MMAP -LARGESEQS=0 -WAIT -DSPBLOCK=0.05 -LONGIGC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : GenEmb1:<sup>\*</sup>

1: gb\_ba:\*
2: gb\_htg:\*
3: gb\_in:\*
4: gb\_om:\*
5: gb\_ov:\*
6: gb\_dat:\*
7: gb\_ph:\*
8: gb\_dl:\*
9: gb\_pr:\*
10: gb\_ro:\*
11: gb\_sts:\*
12: gb\_sy:\*
13: gb\_un:\*
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	605.5	98.3	507	11	G7347	G7347 Ghrelin X1-
2	605.5	98.3	5199	9	AF266558	AF266558 Homo sapi
c 3	605.5	98.3	104947	9	AC008116	AC008116 Homo sapi
c 4	605.5	98.3	146947	2	AC012515	AC012515 Homo sapi

SUMMARIES

AC022384 Homo sapi  
AC012600 Homo sapi  
AC090841 Homo sapi  
AC052274 Macaca mu  
AY372274 Macaca mu  
AY455990 Cervus el  
AY455987 Odocoileu  
ARJ70496 Sequence  
AR208181 Sequence  
AR104108 Sequence  
AX0522356 Sequence  
AX154581 Sequence  
BD061161 Motilin h  
AY184207 Homo sapi  
CQ722673 Sequence  
CQ794618 Sequence  
BD012137 Novel pep  
AB029434 Homo sapi  
AU252278 Homo sapi  
BD222667 Human sig  
AY356127 Sequence  
BC025791 Homo sapi  
BD252557 Sequence  
AY403380 Sequence  
AY464308 Sequence  
AY359053 Homo sapi  
AY455994 S1 Odocoileu  
AY455988 S1 Rangifer  
AC117556 Mus muscu  
AB060078 Mus muscu  
AY089201 Felis cat  
AY455985 Capra hircus  
AB089202 Felis cat  
AY455979 Bos tauru  
AY455981 Koogia bre  
AY455982 Alces alci  
AY454076 Bison bis  
CQ794617 Sequence

## ALIGNMENTS

RESULT 1  
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LOCUS G72347 Ghrelin X1-2 Human Homo sapiens STS 20-JUN-2001  
DEFINITION Ghrelin X1-2 Human Homo sapiens sequence tagged site.  
ACCESSION G72347  
VERSION G72347.1 GI:14518296  
KEYWORDS Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 507)  
AUTHORS Cox,D.G., Boillot,C. and Canzian,F.  
TITLE Genome Survey  
JOURNAL Unpublished (2000)

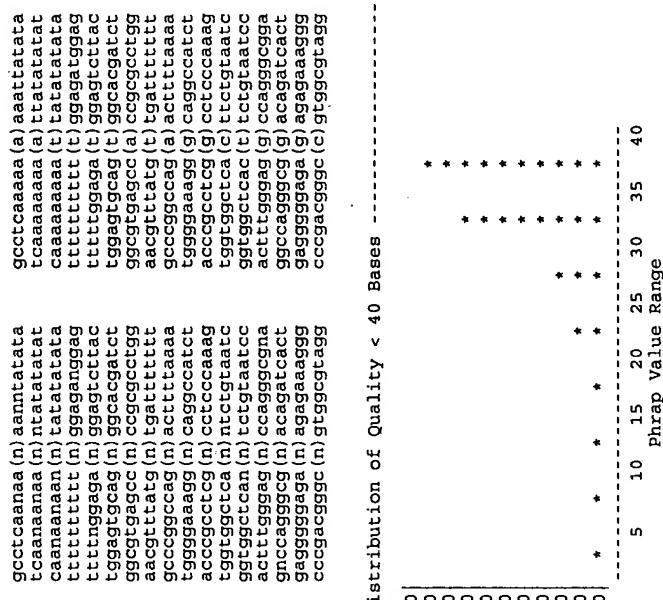
COMMENT

Contact: Federico Canzian  
Genome Analysis Group  
International Agency for Research on Cancer  
150, cours Albert-Thomas, F-69372 Lyon Cedex 08 France  
Tel: +33-4-7238698  
Fax: +33-4-72383888  
Email: canzian@iarc.fr  
Primer A: AGACCTCTTCCCGAG  
Primer B: TCCCTGCTGCCACAGA  
STS size: 507  
Protocol:  
Template: 50 ng

Primer:	4	uM each	AUTHORS	Wajnrajch,M.P., Ten,I.S., Gertner,J.M. and Leibel,R.L.
dNTP:	2	mm each	TITLE	Direct Submission
MgCl2:	1.5-2.5	mm	JOURNAL	Submitted (15-AUG-2000) Pediatrics, Weill Medical College of Cornell University, 525 East 86th Street, Room M-624, New York, NY
Tag:	0.05	units	FEATURES	Location/Qualifiers
Total Vol.:	25	ul		1. .5199
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KCl:	50 mM			/db_xref="taxon:9606"
Tris-HCl:	20 mM			/chromosome=13 "
ph:	8.4			/map="3226-p25"
FEATURES	source			/clone=BAC CTB-187P1"
STS				1. .5199
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primer_bind				/note="GHS"
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				/product="Growth hormone secretagogue precursor"
				1. .554
				/gene="GRELIN"
				/number=1
				1. .446
				/gene="GRELIN"
				join(447..554..749.. .865..3814.. .3922..4732.. .4751)
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				/codon_start=1
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				/protein_id="PAAIG1300..1"
				/db_xref="GI:9966513"
				/translation="MPSSPTVCSILLLGLMLWLILAMAGSSSELSPEHQVRQQRKESKKP
				PDKLQPQRAGWIRPEDQGQAEGADEDELEVRNAFPDVGIKLUSCVQYQHSQLGKF"
				QDIIWEKEAPADK"
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				/gene="GRELIN"
				/note="Octetrahydroxylation; modified site"
				555..748
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				749..865
				/gene="GRELIN"
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				ORIGIN
				Alignment Scores:
				Pred. No.:
				Score:
				Percent Similarity:
				Best Local Similarity:
				Query Match:
				DB:
				Length:
				Matches:
				Conservative:
				Mismatches:
				Indels:
				Gaps:

US-10-659-782a-32 (1-116) x AF296558 (1-5199)	QY	1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuAspIeu 20	AUTHORS Worley, K.C.
	Db	447 ATGCCCTCCAGGACCGTCTGAGCTCTGGCTGCTGGCTGGACTG 506	TITLE Direct Submission
	QY	21 AlamataLaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40	JOURNAL Submitted (09-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
	Db	507 GCGATGGAGGTCAAGTCAGTTCTAGCCTGAACAGAGTCAGCTGACCTCC 566	5 (bases 1 to 104947)
	QY	41 HisysAlaProHisValValProAlaLeuProLeuSerSerAsnGlnLeuCysAspLeuIeu 60	REFERENCE Worley, K.C.
	Db	567 CACAAGCCCCACATGTTTCCAGCCCTGCCACTTAGAACAGCTGTGACCTCGAG 626	AUTHORS Direct Submission
	QY	61 GingInaGhi---TrpAlaSerValPheserGlnSerThrLysAspSerGlySerAsp 79	JOURNAL Submitted (11-JUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
	Db	627 CAGGAGGCCATCTGCTCTGGCTCTAGTCTCTCCAGAsCACAAAGGACTCTGGCTCTGAG 686	6 (bases 1 to 104947)
	QY	80 LeathrValSerGlyArgPhrTrpGlyLeuArgValLeuAspArgLeuProProSer 99	REFERENCE Worley, K.C.
	Db	687 CTCATGTTCTGAGAGCATGGGGCTAGTCTAAACAGACTGTTCCCTCTCC 746	AUTHORS Direct Submission
	QY	100 SerargGluargSerArgargSerHisGlnProSerCysSerProGluIeu 116	JOURNAL Submitted (15-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
	Db	747 AGCGAGAGAAGGACTCGAGAACGCCAACGGCAAGCTGAGCCCCGAGCTC 797	On Sep 30, 1999 this sequence version replaced gi:5882338.
			INFORMATION: http://www.hgsc.bcm.edu/ or email gc-help@bcm.tmc.edu
			CLOSE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
			ANNOTATION OF FEATURES:
			STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
			Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
			Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
			SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
			QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.
			QUALSTAT-REPORT-----
			Contig length: 104947
			Phrap values in estimate: 10425
			Average error rate (BCM-Phrap estimate): 0.000147946
			Fraction of Phrap values less than 40 : 0.0217748
			Number of consensus Changing edits: 21
			Number of N's in consensus : 0
			Summary Statistics -----
			Position Original+Context Edited+Context
			cctgtttttt (t) tttttatgttga
			gcggcgctgg (g) ttacaccctg
			ctggactcca (n) ccctggcaac
			tttgccctcaa (n) aaaaattat

Page 4



Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., John, R., Jolivet, S., Joudah, S., Karissoun, E., Kelly, S., Khan, U., King, L., Korvah, J., Kratovic, J., Kureshi, A., Landry, N., Leah, B., Lewis, L.C., Louis, L., Li, J., Li, Z., Lichatowicz, O., Lieu, C., Liu, J., Liu, W., Lozada, R.J., Lu, X., Lucier, R., Luna, R., Ma, J., Mateshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Nguyen, A., Nguyen, N., Nickerson, E., Nwokonwo, S., Ogwu, M., Okwuonu, G., Organyen, N., Oviied, R., Pace, A., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Siisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamersisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Will, R., Wang, S., Ward-Moore, S., Williamson, A., Washington, S., Williams, G., Williamson, A., Wieczynski, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., and Gibbs, R.

**JOURNAL** Direct Submission  
Unpublished  
2 (bases 1 to 146947)  
Worley, K.C.

**AUTHORS** Direct Submission  
Submitted (29-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jan 7, 2001 this sequence version replaced gi:929498.  
Center: Baylor College of Medicine  
Center Code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: HMLC  
Center clone name: RP11-85J5  
----- Summary Statistics  
Sequencing vector: M13; L08821  
Chemistry: Dye-terminator Big Dye: 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 117566 bases at least Q40  
Consensus quality: 133456 bases at least Q30  
Estimated insert size: 135052; sum-of-contigs estimation  
Estimated insert size: 207623; agarose-fp estimation  
Quality coverage: 2.0x in Q20 bases; sum-of-contigs estimation  
Quality coverage: 3.0x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
(see [http://www.hgsc.bcm.tmc.edu/docs/Genbank/draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank/draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 16 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 42943: contig of 42943 bp in length  
\* 42944 43043: gap of unknown length  
\* 43044 65409: contig of 22366 bp in length  
\* 65509: gap of unknown length  
\* 65510 82660: contig of 17151 bp in length  
\* 82661 96493: contig of 13733 bp in length  
\* 96494 96593: gap of unknown length  
\* 96594 105307: contig of 8714 bp in length  
\* 105308 105407: gap of unknown length  
\* 105408 111881: contig of 6474 bp in length

**TITLE** JOURNAL  
**COMMENT** JOURNAL  
**REFERRERS** JOURNAL  
**FEATURES** Location/Qualifiers  
Source  
1. 146947  
/organism="Homo sapiens"  
/mol type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="3"  
/clone="RP11-85J5"

**ORIGIN**

Alignment Scores:  
Pred No.: 2.9e-40 Length: 146947  
Score: 6550 146947  
Percent Similarity: 99.15% Matches: 116  
Best Local Similarity: 99.15% Conservative: 0  
Query Match: 98.30% Mismatches: 0  
DB: 2 Indels: 1  
Gaps: 1

US-10-659-782A-32 (1-116) x AC012515 (1-146947)

Qy 1 MetProSerProGlyThrValCysSerLeuIleGlyMetLeuTyrPheAspIeu 20  
Db 35989 ATGCCCTCCAGGACCGTCAGCTCTGGATGCTCTGGACTTG 36048

Qy 21 AlaMetAlaGlySerSerPhelSerProGluHiBclnArgVaGlnValArgProPro 40  
Db 36049 GCATGGCAGGGCTCAcGCTCTGGCTCTGAACCAAGAGGTCCGGTGAACCTCC 36108

Qy 41 HisLybAlaProHisValValProAlaLeuProLeuSerArgInLeuCysAspLeuLiu 60  
Db 36109 CRCAAGGCCAACAGTTGTTCAAGCTGCAACAGCTCTGAACTGAG 36168

Qy 61 GluGlnGargHis--TrpAlaSerValPheSerGlnSerThrAspSerGlySerAsp 79  
Db 36169 CAGCAGGCCATCTGGCTTCAGCTCTGGCTTAAGGCTAACAGCTCTGGCTGAC 36228

Qy 80 LeuThrValSerGlyArgThrTrpGlyLeuArgValLeuArgLeuPheProProSer 99  
Db 36229 CTCACTGTTTCAGGAGCATGGGCTTAGGCTAACAGCTCTGGCTGAC 36288

Qy 100 SerArgGluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116  
Db 36289 ACCAGAGAAAGGTGAAAGCCACAGCTGAGCTGAGCCCAGCT 36339

RESULT 5  
AC022384 /C LOCUS AC022384  
DEFINITION Homo sapiens chromosome 3 clone RP11-138J1 map 3P, complete  
ACCESSION AC022384  
VERSION AC022384.5 GI:24418051  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

REFERENCE	AUTHORS	JOURNAL	COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Guo,D., Guo,Z., He,J., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Liu,B., Li,F., Li,G., Li,J., Li,L., Li,T., Liu,Y., Liu,N., Liu,N., Liu,N., Liu,Y., Liu,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,J., Wang,L., Wang,L., Wang,X., Wang,X., Wang,J., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.	Submitted (1-bases 1 to 210053)	Unpublished 3p genomic sequence 2 (bases 1 to 210053)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Guo,D., Guo,Z., He,J., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Liu,B., Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,N., Liu,N., Liu,Y., Liu,W., Li,Y., Luo,C., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yan,C., Yang,X., Zhang,G., Zhang,Y., Zhang,X., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.	Submitted (03-FEB-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing	Submitted (03-FEB-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Guo,D., Guo,Z., He,J., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Liu,B., Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,N., Liu,N., Liu,Y., Liu,W., Li,Y., Luo,C., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L., Wang,L., Wang,X., Wang,X., Wang,J., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.	Direct Submission Submitted (16-JAN-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing	Submitted (16-JAN-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Guo,D., Guo,Z., He,J., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Liu,B., Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,N., Liu,N., Liu,Y., Liu,W., Li,Y., Luo,C., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,L., Wang,L., Wang,X., Wang,X., Wang,J., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.	Direct Submission Submitted (29-OCT-2002) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing	Submitted (29-OCT-2002) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Chen,L., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Guo,D., Guo,Z., He,J., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Liu,B., Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,N., Liu,Y., Liu,W., Li,Y., Luo,C., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J. and Yang,H.	Direct Submission Submitted (08-NOV-2002) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing	Submitted (08-NOV-2002) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing

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AUTHORS	Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodotzky, B., Bouck, J., Bowie, S., Brooks, A., Bunay, C., Bunac, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., David, R., Delgado O., Deshabzo, D., Ding, Y., Domah, Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Forcum-Tansley, J., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, L. L., Guevara, W., Harris, J., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Jackson, L. E., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondelewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichertage, O., Liu, J., Liu, W., Logan, O., Lozano, R., Lu, J., Martin, R., Martinez, C., McLeod, M. P., Mei, G., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, N., Nguyen, S., Obwala, G., Parish, B., Paxton, S., Payron, B., Perez, I., Pu, L. I., Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, B., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Waibah, M., Watlington, S., Weinstock, G., Weinstock, J. R., Williamson, A., Worley, K., Wren, J., Wrenford, G., Yu, W., Zhou, X., Nelson, D., and Gibbs, R.							
TITLE	Unpublished							
REFERENCE	2 (bases 1 to 216292)							
AUTHORS	Worley, K. C.							
JOURNAL	Direct Submission							
COMMENT	Submitted (31-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 4, 2000 this sequence version replaced gi:9719583. Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ----- Project Information Center project name: HMQN Center clone name: RP1-1082A18 ----- Summary Statistics Sequencing vector: M13; L08821 Chemistry: Dye-terminator Big Dye: 98% of reads Assembly program: Phrap; version 0_990329 Consensus quality: 193458 bases at least Q40 Consensus quality: 207037 bases at least Q30 Consensus quality: 210993 bases at least Q20 Estimated insert size: 213807; sum-of-contigs estimation Estimated insert size: 317914; agarose-fp estimation Quality coverage: 3x in Q20 bases; agarose-fp estimation Quality coverage: 4.4x in Q20 bases; sum-of-contigs estimation							
RESULT	NOTE: Estimated insert size may differ from sequence length. * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. * 1 84660: contig of 84660 bp in length * 84661 84760: gap of unknown length * 84761 141893: contig of 57133 bp in length * 141894 141993: gap of unknown length * 141994 157877: contig of 15884 bp in length * 157878 157977: gap of unknown length * 157978 173768: contig of 15791 bp in length * 173769 173868: gap of unknown length	7						
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DEFINITION	Homo sapiens chromosome 3 clone RP1-1082A18 map 3p, complete							
ACCESSION	AC090841							
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ORGANISM	Homo sapiens							
REFERENCE	Zhang, L., Bao, J., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Hu, S., Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, F., Li, G., Li, J., Li, L., Li, S., Li, T., Liu, Y.,	1 (bases 1 to 217778)						



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LCUS	Cervus elaphus canadensis	362 bp	DNA
DEFINITION	Cervus elaphus canadensis	ghrelin gene,	
ACCESSION	AY455990	exons 1, 2 and partial cds.	
VERSION	AY455990.1	GI:45545386	
KEYWORDS	1 of 2		
SEGMENT	Cervus elaphus canadensis (wapiti)		
SOURCE	Cervus elaphus canadensis		
ORGANISM	Cervus elaphus canadensis		

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; Cervinae; Cervus;	REFERENCE 1 (bases 1 to 362)		
AUTHORS Dickin,J.C., Thue,T.D. and Buchanan,F.C.	TITLE An Investigation into the Mammalian Ghrelin Gene		
JOURNAL Unpublished	LOCATION/Qualifiers		
JOURNAL Submitted (02-NOV-2003) Animal and Poultry Science, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada	LOCATION/Qualifiers		
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JOURNAL VERSION AY455987.1			
JOURNAL MAM 23-MAR-2004			
JOURNAL KEYWORDS exons 1, 2 and partial cds.			





Search completed: February 10, 2005, 15:18:58  
 Job time : 3413 secs

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**RESULT 15**

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DEFINITION Sequence 1 from Patent WO0138355.

ACCESSION AX154581

VERSION AX154581.1 GI:14536167

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominoidea; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 Sheppard, P.O., Jaspers, S.R., Deisher, T.A. and Bishop, P.D.

AUTHORS Method of forming a peptide-receptor complex with zsg33 and therapeutic use thereof

TITLE Patent: WO 0138355-A 1 31-MAY-2001;

JOURNAL ZymoGenetics, Inc. (US)

FEATURES Location/Qualifiers

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ORIGIN

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us-10-659-782A-32 (1-116) x AX154581 (1-351)

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Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60

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Aaz8121 Human sig

Aad38238 Human zba

Aad57579 Human zba

Aai58046 Human pol

Aaz65048 Membrane

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Aca64340 Novel hum

Aca3823 cDNA enco

Acd44308 cDNA enco

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OS Homo sapiens.

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No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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PR	11-JUL-2000;	2000US-0217496P.	PR	01-NOV-2000;	2000US-0244617P.
PR	14-JUL-2000;	2000US-0218290P.	PR	08-NOV-2000;	2000US-024474P.
PR	26-JUL-2000;	2000US-0220563P.	PR	08-NOV-2000;	2000US-024475P.
PR	26-JUL-2000;	2000US-0220564P.	PR	08-NOV-2000;	2000US-024476P.
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PR	29-SEP-2000;	2000US-0236369P.	PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.	
PR	02-OCT-2000;	2000US-0236802P.	PT	Disclosure; SEQ ID NO 36846; 3071pp + Sequence Listing; English.	
PR	02-OCT-2000;	2000US-0237037P.	PS	AAK51951 to AK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM9191 to AAM9217 to AAM9191. (I) have cytosolic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome	
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PR	29-SEP-2000;	2000US-0236322P.	Rosen CA, Barash SC, Ruben SM;

DR	WPI; 2001-483426/52.	XX	OS
PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.	XX	Homo sapiens.
PT	XX	XX	WO200157782-A2.
PS	SEQ ID NO 36845; 3071pp + Sequence Listing; English.	XX	PN
XX	XX	PD	09-AUG-2001.
CC	AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequence given in AAM8210 to AAM91921. (I) have Cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64103 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention	XX	PF
XX	XX	17-JAN-2001;	2001WO-US001354.
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 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
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 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
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 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Barash SC, Ruben SM;  
 XX WPT; 2001-483426/52.  
 XX PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.  
 XX PS Disclosure; SEQ ID NO 36842; 3071pp + Sequence Listing; English.  
 XX CC AAK54951 to AAK65702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.  
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 Pred. No.: 3.33e-53 Length: 5036  
 Score: 605.50 Matches: 116  
 Percent Similarity: 99.15% Conservative: 0  
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 Db 4916 CACAAGCCCCACATGGTTCAAGCCCTGGCAACTTAGCAACCGCTCTGAGACTCTGGAG 4857  
 Qy 61 Glu Gln Arg His -- TTPA laser val Phe Ser Gln Ser Thr Lys Asp Ser Gln 79  
 Db 4856 CAGAGGCCATCTGGCTCAGTCCTCAGGCAAGGACTCTGGCTCTGGCT 4797  
 Qy 80 Leu Thr Ile Ser Gly Arg Thr Trp Gly Leu Arg Val Leu Asp Arg Leu Phe Ile Pro Ser Pro Glu Leu 99  
 Db 4796 CTCACTGTTCTGGACATGGGCTTAACAGACTGTTCCCTTC 4737  
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 ID ABA16827 Standard; DNA; 5036 BP.  
 XX AC ABA16827;  
 DT 23-JAN-2002 (first entry)  
 XX

DB Human nervous system related polynucleotide SEQ ID NO 9158.  
 XX Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;  
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;  
 KW antiparkinsonian; antischismic; antianæmic; antiarthritic; cancer;  
 KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;  
 KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal;  
 KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.  
 XX WO200159063-A2.  
 OS Homo sapiens.  
 PN XX  
 PD 16-AUG-2001.  
 XX PR 17-JAN-2001; 2001WO-US001334.  
 XX PR 31-JAN-2000; 2000US-0179065P.  
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PA	(HUMA-)	HUMAN GENOME SCI INC.	XX	
XX	Rosen CA,	Barash SC,	DE	Human nervous system related polynucleotide SEQ ID NO 9159.
PI	WPI;	2001-541565/60.	XX	
XX	DR;		KW	Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
XX			KW	immunosuppressant; antiinflammatory; antiviral; HIV; antibacterial; cancer;
XX			KW	antiparkinsonian; antiseptic; antianaemic; antiarthritic; cancer;
PR			KW	antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
PR			KW	anti-allergic; antidiabetic; anticonvulsant; antifungal;
PR			KW	antiparasitic; cardiotonic; immune disorder; cardiovascular disorder;
XX			KW	neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
PS			XX	
PS	Disclosure;	SEQ ID NO 9158;	1701pp + Sequence Listing; English.	
XX			OS	
CC			XX	
CC	The invention relates to novel genes (ABA11004-ABA21534) and proteins		XX	
CC	(ABB14578-ABB18001) useful for preventing, treating or ameliorating		XX	
CC	medical conditions e.g. by protein or gene therapy. The genes are		XX	
CC	isolated from a range of human tissues and/or treating nervous system cancers		XX	
CC	and metastases.		PD	16-AUG-2001.
CC			XX	
CC	Disclosure; SEQ ID NO 9158; 1701pp + Sequence Listing; English.		PP	17-JAN-2001; 2001WO-US001334.
CC			XX	
CC	The invention relates to novel genes (ABA11004-ABA21534) and proteins		XX	
CC	(ABB14578-ABB18001) useful for preventing, treating or ameliorating		XX	
CC	medical conditions e.g. by protein or gene therapy. The genes are		XX	
CC	isolated from a range of human tissues and/or treating nervous system cancers		XX	
CC	and metastases.		XX	
CC	The nucleic acids, proteins, antibodies and (ant)agonists are useful in		XX	
CC	the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and		XX	
CC	ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,		XX	
CC	breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune		XX	
CC	disorders e.g. Addison's disease, allergies, autoimmune haemolytic		XX	
CC	anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,		XX	
CC	multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)		XX	
CC	cardiovascular disorders such as myocardial ischaemia; (d) wound healing		XX	
CC	; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)		XX	
CC	infectious diseases such as viral, bacterial, fungal and parasitic		XX	
CC	infections. Note: The sequence data for this patent did not form part of		XX	
CC	the printed specification, but was obtained in electronic format directly		XX	
CC	from WIPO at <a href="http://ftp.wipo.int/pub/published_pct_sequences">ftp.wipo.int/pub/published_pct_sequences</a>		XX	
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Alignment Scores:			XX	
Prod. No.:	3.33e-53	Length:	5036	
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Percent Similarity:	99.15%	Conservative:	0	
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Query Match:	98.30%	Indels:	1	
DB:	5	Gaps:	1	
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QY	61 GluGlnArgHis---TriplaaSerValheSerIleSerThrIleSerGlySerAsp	79	PR	0225267P.
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			PR	0231242P.



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QY 80 LeuThrValSerGlyArgThrPheProGlyLeuAsnArgValLeuAsnArgLeuPheProProSer 99  
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 AC ADK66746;  
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 DT 06-MAY-2004 (first entry)  
 XX  
 DE Porcine ghrelin consensus DNA spanning exon 1 and exon 2.  
 KW Growth; appetite; fatness; genotype; polymorphism; ghrelin protein;  
 KW breeding; porcine; db.  
 OS sp.  
 XX  
 FH misc\_feature L\_121  
 FT /tag= a  
 FT /note= "Ghrelin protein"  
 FT misc\_signal 11..13  
 FT /tag= b  
 FT /note= "Initiation codon"  
 FT variation replace(145,A)  
 FT /tag= C  
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 FT /note= "Ghrelin protein"  
 FT variation replace(440,T)  
 FT /tag= f  
 FT /standard\_name= "Single nucleotide polymorphism (SNP)"  
 XX US2003111512-A1.  
 XX 13-NOV-2003.  
 PD XX  
 PP 14-NOV-2002; 2000US-00294131.  
 PR XX  
 PR 14-NOV-2001; 2001US-0333222P.  
 PA (ROTH/) ROTHSCHILD M F.  
 PA (KIMK/) KIM K.  
 PA (ANDE/) ANDERSON L L.  
 PI Rothschild MF, Kim K, Anderson LL;  
 DR WPI: 2004-010667/01.  
 XX  
 PR screening animals (i.e. pigs) to determine those more likely to produce desired growth, appetite and fatness to optimize breeding and selection techniques comprises detecting the presence of a polymorphism in the Ghrelin gene.  
 XX Disclosure: SEQ ID NO 11; 24pp; English.  
 XX The present invention relates to a method of screening animals to determine those more likely to produce desired growth, appetite and fatness which involves obtaining a sample of genetic material from the

CC animal and assaying for the presence of a genotype in the animal which is associated with favourable growth, appetite and fatness, the genotype characterised by a polymorphism in the Ghrelin gene. The composition and methods are useful in screening animals (i.e. pigs) to determine those more or less likely to produce desired growth, appetite and fatness to optimise breeding and selection techniques. The present sequence is porcine ghrelin consensus DNA spanning exon 1 and exon 2 of the invention.

XX SQ Sequence 447 BP; 93 A; 133 C; 140 G; 81 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 5.9e-14 Length: 447  
 Score: 220.00 Matches: 65  
 Percent Similarity: 57.81% Conservative: 9  
 Best Local Similarity: 50.78% Mismatches: 36  
 Query Match: 35.71% Indels: 18  
 DB: 12 Gaps: 5

US-10-659-782A-32 (1-116) x ADK66746 (1-447)

QY 1 MetProSerProGlyLysValCysSerIleLeuGlyMetLeuIlePhe---Asp 19  
 DB 11 ATGCCCTCACGGGACCATTCAGCTGCCTCCAGCTGCTCCTAGCGAC 70

QY 20 LeuAlaMetAlaGlySerSerPheLeuSerProGluLysGluArgValnValArgPro 39  
 DB 71 TTGGCCATGGCGCTCCAGCTCTTCAGCCCAGAACCCAGAAAGTCAGCTAAGACT 130

QY 40 ProHisLysAlaPro-----HisValValProAlaLeuProLeuSerArgCln 55  
 DB 131 CTCCCCAGAGCCCCGGCTTAGCTCATCCAGCCTCTCCATGAGTTGGGACC 190

QY 56 LeuCysAspLeuGluGlnGlnArgHsLeuPheSerGlnSer---ThrIysA 75  
 DB 191 TGGCTAACCTG-----CTCTGGCTTCAGCCCTCTCCAGGAGCACTCTGG 238

QY 75 sp--SerGlySerAspLeuThrVal-----SerGlyArgThrTyrG 88  
 DB 239 ATCTGGCAAGGGGCCATACCTTGCTGCTGCTGGAGGAGTAGCTGGGGTGGCGG 298

QY 88 IleLeuArgValLeuAspArgLeuIlePheProProSerSerArgSerH 108  
 DB 299 CATCTTAAGGGCCCTCAAGAGGAGCTTCCTCTCCAGCAGAAAGGAGTCCCAAAGGCC 358

QY 108 iLeuInProSerCysSerPro 114  
 DB 359 AGCAGCCAAACTGAAGCCC 378

RESULT 8  
 AAX04550  
 ID AAX04550 standard; cDNA; 351 BP.  
 XX  
 AC AAX04550;  
 XX  
 DT 07-APR-1999 (first entry)  
 XX  
 DE CDNA encoding a protein designated zsig33.  
 XX  
 KW Zsig33; gastric motility; gastrointestinal inflammation; reflux disease;  
 KW nutrient absorption regulation; obesity; metabolic disorder; ss.  
 XX  
 OS Homo sapiens.

XX Key  
 FH Location/Qualifiers  
 FT 1..351  
 FT /\*tag= a  
 FT /note= "no termination codon"  
 FT sig\_peptide 1..69  
 FT /\*tag= b  
 FT mat\_peptide 70..351  
 FT /\*tag= c

PN	WO9842840-A1.		RESULT 9
XX	PD 01-OCT-1998.	AAF30033	AAF30033 standard; DNA; 351 BP.
XX	PF 23-MAR-1998;	ID	AAF30033
XX	98WO-US005620.	XX	
XX	AC AAF30033;	AC	
PR 24-MAR-1997;	97US-0041102P.	XX	
PR 24-MAR-1997;	97US-00822897.	XX	
PA (ZYMO ) ZYMOGENETICS INC.		DT	23-APR-2001 (first entry)
XX	Sheppard PO, Deisher TA;	XX	DNA encoding zsig33.
XX	PI WPI; 1999-070071/06.	XX	SGIP; zsig33; human; chromosome 3p26.1; anorectic; antidiabetic; nutritional absorption modulator; growth hormone secretagogue; somatotropin; somatomedin-C; gene therapy; ss.
DR P-PSDB; AAW8791.		XX	KW
XX	Human polypeptide having homology to motilin, zsig33 - useful e.g. to treat gastrointestinal motility disorders, obesity etc. and to identify antagonists to treat gastrointestinal hypermotility.	XX	KW
PS Claim 5 : Page 54-55; 6pp; English.		XX	Homo sapiens.
CC The present sequence encodes a protein designated zsig33. The nucleic acids are strongly expressed in stomach tissue. The polypeptide (or allelic variants/orthologs) can be used to stimulate gastric motility, measured as increased transit time or gastric emptying of an ingested substance in mammals. The products are used to treat disorders associated with gastrointestinal cell contractility, secretion of digestive enzymes/acids, gastrointestinal motility, recruitment of digestive enzymes, gastrointestinal inflammation, reflux disease and nutrient absorption regulation. Zsig33 polypeptides may also be important neurologically, since the family of gut-brain peptides to which the homologous protein motilin belongs has been associated with neurological and CNS functions. They may therefore be used e.g. to regulate satiety or treat obesity and other metabolic disorders where neurological feedback modulates nutritional absorption. They are useful to identify zsig33		OS	
CC agonists, antagonists and ligands, and to produce antibodies		XX	Location/Qualifiers
XX	Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;	XX	1. .69
XX	Alignment Scores:	XX	/*tag= a
Pred. No. :	1.84e-13	Length:	70. .351
Score:	214.00	Matches:	b
Percent Similarity:	44.44%	Conservative:	
Best Local Similarity:	43.59%	Mismatches:	
Query Match:	34.74%	Indels:	
DB:	2	Gaps:	
US-10-659-782A-32 (1-116) x AAX04550 (1-351)			
Qy 1 MetProSerProGlyThrValCysSerIleLeuIleLeuIleGlyMetLeuTrpLeuAspIleuLeu 20			
Db 1 ATGCCCTCCCAGGGACGTCTGCAGCTCCCTGGATCTGGCTGGACTTG 60			
Qy 21 AlaMetAlaGlySerSepPhelLeuSerProGluHisGlnArgValGlnValArgProPro 40			
Db 61 GCGATGGAGGCTCCAGCTTCTGACCAAGGAGTC 108			
Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60			
Db 108 ----- 108			
Qy 61 GluGlnIleGlyIleAspSerValPheSerGlnSerThrLysAspSerGlySerAspIleu 80			
Db 108 ----- 108			
Qy 81 ThrValSerArgArgThrTrpGlyLeuArgValLeuIleAsnArgLeuPheProProSerSer 100			
Db 108 ----- 108			
Qy 1 MetProSerProGlyIleGlySerIleLeuIleGlyMetLeuTrpLeuAspIleuLeu 20		Length:	351
Db 1 ATGCCCTCCCAGGGACGTCTGCAGCTCCCTGGATCTGGCTGGACTTG 60		Matches:	51
Qy 101 Arg-Glu-LysSerArgArgSerHisGlnProSerCysSerProGluIleu 116		Conservative:	1
Db 109 CAGAGAAAGGAGTCGAGAACGCCACGCCAGCTGAGCCCCAGTC 157		Mismatched:	0
Qy 101 Arg-Glu-LysSerArgArgSerHisGlnProSerCysSerProGluIleu 116		Indels:	65
Db 109 CAGAGAAAGGAGTCGAGAACGCCACGCCAGCTGAGCCCCAGTC 157		Gaps:	1
US-10-659-782A-32 (1-116) x AAX04550 (1-351)			
Qy 1 MetProSerProGlyIleGlySerIleLeuIleGlyMetLeuTrpLeuAspIleuLeu 20			
Db 1 ATGCCCTCCCAGGGACGTCTGCAGCTCCCTGGATCTGGCTGGACTTG 60			

QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHiGlnArgValGlnValArgProPro 40  
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 Db 61 GCGATGGAGCTCCAGTTCAGCTCCAGCTGAACCCAGAGGCCAG 108

QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60  
   108 -----

Db 61 GlnGlnArgHistrpPalaservalPheSerGlnSerThrLysAspSerAsp 80  
   108 -----

QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100  
   108 -----

Db 108 -----

QY 101 Arg-GluArgSerArgArgSerHiGlnProSerCysSerProGluLeu 116  
   :: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 Db 109 CAGGAAAGGAGTCAAGTGAAAGGCCACCCAGCAAAAGTCGCACCCCAGCTC 157

RESULT 10  
 AAF83678 ID AAF83678 standard; CDNA; 351 BP.  
 XX AC AAF83678;  
 XX DT 23-JUL-2001 (first entry)  
 XX DS Human zsig33 polypeptide encoding cDNA.  
 XX KW zsig33; signal transduction; hormone; enzyme; neural development;  
 KW gastric contractility; nutrient uptake; digestive; pancreatic; human;  
 KW insulin-like growth factor-1; growth hormone; bone; gastrointestinal;  
 KW glucose; osteopathic; anorectic; pulmonary; immunomodulator; GHS-R;  
 KW G-protein coupled receptor; 88.  
 XX OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FR CDS 1..351  
 FR /tag= "zsig33"  
 FR /product= "zsig33"  
 FR /note= "the stop codon is not indicated"  
 PN WO200108355-A2.  
 XX PD 31-MAY-2001.  
 XX PP 22-NOV-2000; 2000WO-US032074.  
 XX PR 22-NOV-1999; 99US-0166765P.  
 XX PA (ZYMO ) ZYMOGENETICS INC.  
 XX Sheppard PO, Jaspers SR, Deisher TA, Bishop PD;  
 XX DR P-PSDB; AAB52649.  
 XX PR Forming reversible peptide receptor complex for purifying cell and  
 PR peptides; stimulating signal transduction and modulating hormone  
 PR secretion, involves contacting a receptor with zsig33 polypeptide.  
 XX PS Example 2; Page 93-94; 11pp; English.

CC pancreatic enzymes and hormones, secretion of insulin-like growth factor  
 CC -I, secretion of non-zsig33 proteins. It is useful for modulating growth  
 CC hormone secretion in a mammal having a disease associated with abnormal  
 CC levels of growth hormone, such as osteoporosis, bone repair, bone  
 CC remodeling, low osteoblast levels, cartilage repair and remodeling,  
 CC skeletal dysplasia, immune suppression, obesity. Growth retardation,  
 CC protein catabolic responses after surgery, cachexia, protein loss  
 CC dwarfism, wound healing and ovulation induction, treating a mammal having  
 CC a metabolic disorder requiring neurological feedback, such as statin  
 CC regulation, glucose absorption and metabolism and neuropathy-associated  
 CC gastrointestinal disorders, and stimulating glucose-induced insulin  
 CC release in a mammal. The present sequence represents the cDNA encoding  
 CC the human zsig33 polypeptide, a peptide ligand for the G-protein coupled  
 CC receptor, GHS-R.

XX SQ Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1 MetProSerProGlyThrValCysSerIleLeuLeuGlyMetIleTrpLeuAspIeu 20  
 Score: 214.00 Length: 351  
 Percent Similarity: 44.44% Matches: 51  
 Best Local Similarity: 43.59% Conservative: 1  
 Query Match: 34.74% Mismatches: 0  
 DB: 4 Indels: 65  
 Gaps: 1

US-10-659-782A-32 (1-116) x AAF83678 (1-351)

QY 1 MetProSerProGlyThrValCysSerIleLeuLeuGlyMetIleTrpLeuAspIeu 20  
 Db 1 ATGCCCTCCCAAGGACCGTCAGCTGCAGCTCCCTGCATGCTGACTTG 60

QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHiGlnArgValArgProPro 40  
 Db 61 GCGATGGAGGTCTCAGTTCCCTGAGCTGACACCAGAGCTCCAG----- 108

QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnClnLeuCysAspLeuGlu 60  
 Db 108 ----- 108

QY 61 GlnGlnArgHistrpAlaSerValPheSerGlySerAspIeu 80  
 Db 108 ----- 108

QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100  
 Db 108 ----- 108

RESULT 11  
 ABV72214 ID ABV72214 standard; DNA; 351 BP.  
 XX AC ABV72214;  
 XX DT 05-DEC-2002 (first entry)  
 XX DE Nucleotide sequence of a human zsig33.  
 XX KW Short gastrointestinal peptide; SGIP; zsig33; motilin; gene; 88.  
 XX OS Homo sapiens.

Location/Qualifiers  
 1..351  
 /\*tag= "zsig33"  
 /product= "zsig33"  
 /note= "no termination codon given"  
 1..69  
 /\*tag= b  
 70..3510

The invention relates to a method of forming a reversible peptide-receptor complex that involves providing an immobilized receptor, and contacting the receptor with a zsig33 peptide (comprising residues 24-37 of AAB52649), where the receptor binds to the zsig33 peptide. The method is useful for purifying cells expressing a peptide, stimulating signal transduction in a cell expressing a receptor. It is also useful for modulating secretion of hormones, neural development and/or utilization, gastric contractility, nutrient uptake, secretion of digestive and



1 ATGCCCTCCAGGGACCGTCTGCAGCCCTCGCTGGCATGCTCTGGCTGGACTTG 60  
 21 AlaMetAlaLysSerSerPheLeuSerProGlutGlnArgValGlnValArgPro 40  
 61 GCCATGGCAGGCTCCAGCTCTAGCCCTGAACACCAGAGTCAG 108  
 41 HisLysAlaProHisValValProLeuSerAsnGlnLeuCysAspLeuIu 60  
 108 -----  
 61 GlnGlnArgHistrpAlaSerValPheSerGlnSerThrLysAspSerAspIeu 80  
 108 -----  
 81 ThrValSerCysArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProSer 100  
 108 -----  
 108 -----  
 Db 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluIeu 116  
 Qy ::|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 109 CAGGAAAGAGAGTCGAAGAGCCACCAAGCAAGTGCAGCCCCAGCTC 157  
 RESULT 13  
 ADN11752 standard; cdNA; 351 BP.  
 ID ADN11752  
 XX  
 AC ADN11752;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DB Human zsig33 coding sequence.  
 XX  
 KW ss; gene; human; zsig33; body weight; body mass; antibody; antagonist;  
 KW gastrointestinal; antiinflammatory; antiulcer; vulnary;  
 KW growth hormone secretagogue; GHS-R; peptide-antibody complex.  
 XX  
 OS Homo sapiens.  
 XX  
 Key  
 CDS 1..351  
 FT /\*tag= a  
 FT /product= "zsig33"  
 FT /partial  
 FT /note= "no stop codon"  
 XX  
 WO2004033645-A2.  
 XX  
 PD 22-APR-2004.  
 XX  
 PP 06-OCT-2003; 2003WO-US031804.  
 XX  
 PR 07-OCT-2002; 2002US-041691BP.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Jaspers SR, Sheppard PO, Bishop PD, Kuijper JL, Deisher TA,  
 XX  
 DR WI; 2004-340913/31.  
 DR P-PSDB; ADN11753.  
 XX  
 PR Use of a zsig33 peptide for e.g. forming a peptide-antibody complex,  
 PR inhibiting signal transduction in a cell expressing a growth hormone  
 PR secretagogue receptor, or treating a metabolic disorder.  
 PS Example 2: Page 88; 100pp; English.  
 XX  
 CC The present invention relates to the use of a zsig33 peptide for forming  
 CC a peptide-antibody complex, purifying a peptide, inhibiting signal  
 CC transduction in a cell expressing a growth hormone secretagogue receptor  
 CC (GHS-R), decreasing fat deposition in a mammal, suppressing the appetite  
 CC of a mammal, inhibiting growth hormone secretion in pituitary cells of a  
 CC mammal, or treating a metabolic disorder. The peptide is useful for  
 CC forming a peptide-antibody complex, purifying a peptide, inhibiting  
 CC signal transduction in a cell expressing a growth hormone, decreasing fat  
 CC deposition in a mammal, suppressing the appetite of a mammal, or inhibiting  
 CC growth hormone secretion in pituitary cells of a mammal, or treating a  
 CC metabolic disorder. The zsig33 polypeptides can be used to study  
 CC proliferation or differentiation in stomach, lung, pituitary,  
 CC hypothalamus, hippocampus, kidney, duodenum, jejunum, small intestine,  
 CC skeletal muscle or pancreas. They are also useful in delivering  
 CC therapeutic agents. Zsig33 polypeptides, agonists and antagonists  
 CC are also useful for promoting wound healing. The polypeptides, nucleic acids  
 CC and antibodies are useful for diagnosing, treating or preventing  
 CC disorders associated with gastric reflux, gastroparesis, modulation of  
 CC secretion of pituitary hormones, including growth hormone, Crohn's  
 CC disease, metabolic wasting, gastric ulcers, weight management, or  
 CC degenerative disease. The present sequence is the human zsig33 coding  
 CC sequence.

XX  
 SQ Sequence 351 BP; 82 A; 107 C; 107 G; 55 T; 0 U; 0 Other;  
 XX  
 Alignment Scores:  
 Pred. No.: 1.84e-13  
 Score: 214.00  
 Length: 351  
 Matches: 51  
 Percent Similarity: 44.44%  
 Best Local Similarity: 43.59%  
 Query Match: 34.74%  
 DB: 12  
 Gaps: 1  
 US-10-659-782A-32 (1-116) x ADN11752 (1-351)  
 Qy 1 MetProSerProGlyThrValCysSerLeuLeuGlyMetLeuTriPheAspLeu 20  
 Db 1 ATCCCTCCCAAGGACGGCTCTGCAGCTCTCCCTGGCATGCTCTGACTTG 60  
 Qy 21 AlaMetAlaGlySerSerPhaLeuSerProGluHisGlnArgValArgProPro 40  
 Db 61 GCCATGGCAGGCTCACCTTCCCTGAGCACCAGAGTCCAG----- 108  
 Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60  
 Db 108 -----  
 Qy 61 GlnGlnArgHistrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80  
 Db 108 -----  
 Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100  
 Db 108 -----  
 Qy 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116  
 Db 109 CAGAGAAGGAGTCGAAGGCAAGCCAGGCAAGCTGAGCTGAGCTC 157  
 RESULT 14  
 AD50726 standard; DNA; 401 BP.  
 ID AD50726;  
 XX  
 AC AD50726;  
 XX  
 DT 02-APR-2003 (first entry)  
 XX  
 DE Human exon 3-deleted ghrelin DNA.  
 XX  
 KW Ghrelin; preproghrelin; GHS-R 1b; benign prostatic hyperplasia; therapy;  
 KW breast; cervical; uterine; choriocarcinoma; prostate; ovary; cytostatic;  
 KW cancer; human; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 CC Location/Qualifiers  
 CC 33 ..308  
 CC /\*tag= ^  
 CC /product= "Human exon 3-deleted ghrelin protein"

PN	WO200290387-A1.	XX	XX	24-APR-2001	(first entry)
PD	14-NOV-2002.	XX	DT		
XX	2002WO-AU000582.	XX	XX		
PF	10-MAY-2002; 2002WO-AU000582.	XX	DB		
XX		XX			
PR	10-MAY-2001; 2001AU-00004919.	XX	KW	Growth hormone secretagogue; GHS; ghrelin; precursor; preproprotein;	
PR	17-DEC-2001; 2001AU-00009567.	XX	KW	calcium concentration elevation; infant growth disorder;	
XX		XX	KW	growth hormone deficiency; ss.	
PA	(UYQU-) UNIV QUEENSLAND TECHNOLOGY.	XX	OS	Homo sapiens.	
XX		XX	OS		
PI	Chopin LK, Jeffery PL, Herrington AC;	XX	PN	WO200107475-A1.	
XX		XX	PN		
WPI:	2003-111957/10.	DR	PD	01-FEB-2001.	
DR	P-PSDB; AAB33410.	XX	XX	24-JUL-2000; 2000WO-JP004907.	
XX		XX	PP		
PT	Identifying a cancer cell or tissue for treating prostate, ovarian, breast cancer, or benign prostatic hyperplasia, by detecting the expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids.	PT	XX	23-JUL-1999; 99JP-00210002.	
PT		PT	PR	29-NOV-1999; 99JP-00338841.	
PT		PT	PR	26-APR-2000; 2000JP-00126623.	
XX		XX	XX		
PS	Example 1; Fig 1; 50pp; English.	PS	PA	(KANG,) KANGAWA K.	
XX		XX	PA		
CC	The invention relates to a method for identifying a cancer cell or tissue of the reproductive system by detecting expression of a ghrelin, an exon-3 deleted preproghrelin and/or a GHS-R 1b proteins or nucleic acids. The antibodies, exon-3 deleted form of preproghrelin and antagonists are useful for treating cancer of the reproductive system such as prostate, ovarian, breast, cervical or uterine cancer, choriocarcinoma or benign prostatic hyperplasia. The present sequence is human exon 3-deleted ghrelin DNA.	CC	PI	Kangawa K., Kojima M., Hosoda H., Matsuo H., Minamitake Y;	
CC		CC	XX		
CC	WPI: 2001-159704/16.	DR	XX		
CC	P-PSDB; AAB60511.	DR	XX		
CC	New peptide compounds which induce growth hormone secretion and elevate cell calcium concentrations, useful in treatment and diagnosis of infant growth disorders.	XX	XX		
CC		XX	PS	Claim 42; Page 183-184; 210pp; Japanese.	
CC		XX	XX		
CC	The invention relates to a novel peptide compound or its salt which induces the secretion of growth hormone and/or elevates calcium ion concentration in cells. The peptides are ghrelin homologues and are characterised in that at least one amino acid has been substituted by a modified amino acid and/or a non-amino acid compound. The invention also encompasses the unmodified peptides; the DNA encoding the peptides; vectors and host cells comprising such DNA; a method of producing the peptides comprising recombinant production, optionally followed by chemical modification; an antibody specific for a peptide of the invention; and an assay and kit for detecting the peptides. The peptides of the invention are useful for treating and/or diagnosing diseases caused by a deficiency in growth hormone expression or activity. In particular, they are useful for promoting infant growth due to growth hormone deficiency. The compounds of the invention are safe with no accompanying side effects. The present sequence represents cDNA encoding a ghrelin-type growth hormone secretagogue (GHS) precursor protein of the invention.	CC			
CC		XX	XX		
SQ	Sequence 401 BP; 92 A; 129 C; 108 G; 72 T; 0 U; 0 Other;	SQ	Sequence 494 BP; 111 A; 156 C; 138 G; 89 T; 0 U; 0 Other;		
Alignment Scores:					
Pred. No.:	2.2e-13	Length:	401	Alignment Scores:	
Score:	214.00	Matches:	51	Pred. No.:	2.89e-13
Percent Similarity:	44.44%	Conservative:	1	Score:	214.00
Best Local Similarity:	43.59%	Mismatches:	0	Percent Similarity:	44.44%
Query Match:	34.74%	Indels:	65	Best Local Similarity:	43.59%
DB:	8	Gaps:	1	Query Match:	34.74%
US-10-659-782A-32 (1-116) × AAD50726 (1-401)		DB:	DB:	DB:	DB:
Qy	1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu	20	Qy	1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu	20
Db	33 ATGCCCTCCCACGGACGTCAGCTCCGTGGCATGCTGGCTGGACTTG	92	Db	34 ATGCCCTCCCACGGACGTCAGCTCCGTGGCATGCTGGACTTG	93
Qy	21 AlaMetAlaGlySerSerLeuSerProGluLysGlnArgValGlnValArgProPro	40	Qy	21 AlaMetAlaGlySerSerLeuSerProGluLysGlnArgValGlnValArgProPro	40
Db	93 GCGATGGGGTCCAGTTCTGAGCTGAACTCAAGCTGGCTGGCTGG	140	Db	94 GCGATGGCAGGTCAAGCTCTGACCCCTGAACACCAGAGTCAG	141
Qy	41 HisLysAlaProHisValValProAlaLeuProLeuSerAanGlnLeuCyBaspLeuGlu	60	Qy	41 HisLysAlaProHisValValProAlaLeuProLeuSerAanGlnLeuCyBaspLeuGlu	60
Db	140 -----	140	Db	140 -----	140
Qy	61 GlnGlnArgHistrpAlaSerValPheSerGlySerAspLeuIle	80	Qy	61 GlnGlnArgHistrpAlaSerValPheSerGlySerAspLeuIle	80
Db	140 -----	140	Db	140 -----	140
Qy	81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer	100	Qy	81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer	100
Db	140 -----	140	Db	140 -----	140
Qy	101 Arg-Glu-Larg-Ser-Arg-Arg-Gly-Ser-His-Gln-Pro-Ser-Cys-Ser-Pro-Glu	116	Qy	101 Arg-Glu-Larg-Ser-Arg-Arg-Gly-Ser-His-Gln-Pro-Ser-Cys-Ser-Pro-Glu	116
Db	141 CAGAGAAGGAGTCGAAGAACGCCACCAAGCTGAGCCCCGAGCTC	189	Db	141 CAGAGAAGGAGTCGAAGAACGCCACCAAGCTGAGCCCCGAGCTC	189
RESULT 15			Qy	21 AlaMetAlaGlySerSerLeuSerProGluLysGlnArgValGlnValArgProPro	40
AF59615			Db	94 GCGATGGCAGGTCAAGCTCTGACCCCTGAACACCAGAGTCAG	141
XX			Qy	41 HisLysAlaProHisValValProAlaLeuProLeuSerAanGlnLeuCyBaspLeuGlu	60
AC					

---

Db	141	-----	-----	-----	141
Qy	61	GlnGlnArgHistrpAla	serValPheSerGlnSerThrLysAspSerGlySerAspIeu	80	
Db	141	-----	-----	-----	141
Qy	81	ThrValSerGlyArgThrTrpGlyLeu	ArgValLeuAsnArgLeuPheProProSerSer	100	
Db	141	-----	-----	-----	141
Qy	101	Arg-Glu	ArgSerArgSerHisGlnProSerCysSerProGluLeu	116	
Db	142	::: CAGA	GAAAGGTGGAAAGGCCACCAAGCTGCAGCCCCAGCTC	190	

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(without alignments)

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-LIST=45 -DOCALLIGN=200 THRESHOLD=100 MAX=100 MIN=0 -THRESHOLD=100 MAX=100 MIN=0 -ALIGNN=15
-NODE=LOCAL -OUTFILE=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=1000000000
-USER=US10659782 @CGN 1 1 69 @runat_05022005_161918_4299 -NCPU=6 -ICPU=3
-NO_MMAR -LARGEQUERY -NEC_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -TREADS=1 -XGAP0=6 -FGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : Issued Patents NA:  
1: /cgn2\_6\_ptoada/1/ina5A\_COMB.seq: \*  
2: /cgn2\_6\_ptoada/1/ina5B\_COMB.seq: \*  
3: /cgn2\_6\_ptoada/1/ina6A\_COMB.seq: \*  
4: /cgn2\_6\_ptoada/1/ina6B\_COMB.seq: \*  
5: /cgn2\_6\_ptoada/1/ina7CUTUS\_COMB.seq: \*  
6: /cgn2\_6\_ptoada/1/ina/backfile.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.4	34.7	351	3	US-09-046-479-1
2	21.4	34.7	351	3	US-09-822-897C-1
3	21.4	34.7	351	4	US-09-608-810A-3
4	21.4	34.7	351	4	US-09-404-417A-1
5	21.4	34.7	654	4	US-10-140-002-441
6	91.5	14.9	9377	4	US-09-801-874-3
C	7	87	14.1	969	4
C	8	87	14.1	2266	2
C	9	85	13.8	536165	4
C	10	82.5	13.4	867	4
C	11	82.5	13.4	2103	4
C	12	82.5	13.4	3222	4

%  
SUMMARIES

Sequence 2, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 179, Ap  
Sequence 17001, A  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 11, Appli  
Sequence 962, App  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 284B, Ap  
Sequence 2774, Ap  
Sequence 55, Appli  
Sequence 1, Appli  
Sequence 2337, Ap  
Sequence 2576, Ap  
Sequence 3809, Ap  
Sequence 3833, Ap  
Sequence 8, Appli  
Sequence 4, Appli  
Sequence 6, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 21, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 29, Appli  
Sequence 6, Appli  
Sequence 7, Appli  
Sequence 7, Appli

ALIGNMENTS

```
RESULT 1
US-09-046-479-1
Sequence 1, Application US/09046479
Patent No. 6291653
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Discher, Theresa A.
TITLE OF INVENTION: MOTILIN HOMOLOGS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,479
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE DOCKET NUMBER: 97-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
TELEX:
```

SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US-08-822,897C  
 FILING DATE:  
 CLASSIFICATION: 536  
 PRIORITY APPLICATION NUMBER:  
 MOLECULE TYPE: cDNA  
 TOPOLOGY: linear  
 STRANDEDNESS: single  
 LENGTH: 351 base pairs  
 TYPE: nucleic acid  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sawislak, Deborah A.  
 REGISTRATION NUMBER: 37,438  
 REFERENCE/DOCKET NUMBER: 97-04  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-442-6672  
 TELEX:  
 FILING DATE:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 351 base pairs  
 STRANDEDNESS: single  
 TYPE: nucleic acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: Coding Sequence  
 LOCATION: 1..351  
 OTHER INFORMATION:  
 NAME/KEY: 819\_peptide  
 LOCATION: 1..69  
 OTHER INFORMATION:  
 NAME/KEY: mat\_peptide  
 LOCATION: 70..351  
 OTHER INFORMATION:  
 US-09-046-479-1  
 Alignment Scores:  
 Pred. No.: 5.14e-17 Length: 351  
 Score: 214.00 Matches: 51  
 Percent Similarity: 44.44% Conservative: 1  
 Best Local Similarity: 43.59% Mismatches: 0  
 Best Local Similarity: 34.74% Indels: 65  
 Query Match: 3 Gaps: 1  
 DB:  
 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTriPheLeu 20  
 1 ATGCCCTCCAGGAGCCGCTGGACCTCTGCATGCTGGTGGACTTG 60  
 Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisClnArgValGlnValArgProPro 40  
 61 GCCATGGCGCTCGAGCTCTGAGCCCTGAGCCCTGAGCAAGTCAG 108  
 Db 41 HisLysAlaProHisValValProAlaLeuSerAsnGlnIeuCysAspLeuGlu 60  
 108 -  
 Qy 61 GlnGlnArgHisTrpAlaSerValPheSerGlnSerThrLysAspSerAspLeu 80  
 108 -  
 Db 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100  
 108 -  
 Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116  
 :: 109 CAGAGAAAGGGTCAAGAACCCACCGCCAAAGCTGAGCCCCGAGCTC 157  
 RESULT 2  
 US-08-822-897C-1  
 Sequence 1, Application US/08822897C  
 Patent No. 6380158  
 GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 APPLICANT: Deisher, Theresa A.  
 TITLE OF INVENTION: MORLIN HOMOLOGS  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Disquette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 RESULT 3  
 US-09-608-810A-3  
 Sequence 3, Application US/09608810A  
 Patent No. 6420521

GENERAL INFORMATION:  
; APPLICANT: Shppard, Paul O.  
; APPLICANT: Jaspers, Stephen R.  
; APPLICANT: Deisher, Theresa A.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: SGIP PEPTIDES  
; FILE REFERENCE: 99-51  
; CURRENT APPLICATION NUMBER: US/09/608, 810A  
; CURRENT FILING DATE: 2000-05-30  
; PRIORITY NUMBER: 60/141,592  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO: 3  
; LENGTH: 351  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(351)  
; NAME/KEY: sig\_Peptide  
; LOCATION: (1)...(69)  
; NAME/KEY: mat\_Peptide  
; LOCATION: (70)...(351)  
; US-09-608-810A-3

Alignment Scores:  
Pred. No.: 5.14e-17 Length: 351  
Score: 214.00 Matches: 51  
Percent Similarity: 44.44% Conservative: 1  
Best Local Similarity: 43.59% Mismatches: 0  
Query Match: 34.74% Indels: 65  
DB: 4 Gaps: 1

US-10-659-782A-32 (1-116) x US-09-404-417A-1 (1-351)

Qy 1 MetProSerProGlyThrValCysSerIleLeuLeuGlyMetLeuTrpLeuAspLeu 20  
Db 1 ATGCCCTCCAGGGACCGTCTGAGCTCTGGATGCTGGCTGACTG 60

Qy 21 AlaMetAlaGlySerSerProGluHisGlnArgValArgProPro 40  
Db 61 GGCATGGAGGCTCACTGAGCTGAGACCCAGAGTCAG 108

Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60  
Db 108 ----- 108

Qy 61 GlnGlnArgHistrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80  
Db 108 ----- 108

RESULT 5  
US-10-659-782A-32 (1-116) x US-09-608-810A-3 (1-351)

Qy 1 MetProSerProGlyThrValCysSerIleLeuLeuGlyMetLeuTrpLeuAspLeu 20  
Db 61 GGCATGGAGGCTCACTGAGCTCTGGATGCTGGCTGACTG 60

Qy 21 AlaMetAlaGlySerSerProGluHisGlnArgValArgProPro 40  
Db 61 GGCATGGAGGCTCACTGAGCTGAGACCCAGAGTCAG 108

Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuL 60  
Db 108 ----- 108

Qy 61 GlnGlnArgHistrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80  
Db 108 ----- 108

Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100  
Db 108 ----- 108

Qy 101 Arg-Glu-Lys-Ser-Arg-His-Gln-Pro-Ser-Cys-Ser-Pro-Glu-Leu 116  
Db 109 CAGGAARGAGTCGAAGCCACCCAACTGGCGCCGGAGCTC 157

RESULT 5  
US-10-140-002-441  
; Sequence 441, Application US/10140002  
; Patent No. 6725730  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerittsen, Mary E.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
; FILE REFERENCE: P330R1C59  
; CURRENT APPLICATION NUMBER: US/10/140,002  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550

RESULT 4  
US-09-404-417A-1  
; Sequence 1, Application US/0940417A  
; Patent No. 6627729  
; GENERAL INFORMATION:  
; APPLICANT: Shppard, Paul O.  
; APPLICANT: Deisher, Theresa A.  
; APPLICANT: Jaspers, Stephen R.  
; TITLE OF INVENTION: TML PEPTIDES  
; FILE REFERENCE: 97-04CL  
; CURRENT APPLICATION NUMBER: US/09/404, 417A  
; CURRENT FILING DATE: 1999-09-23  
; NUMBER OF SEQ ID NOS: 13



Qy 72 SerThrLysAspSerGlySerLeuThrValSerLeuThrGlyArgThrTrpGlyLeuArgVal 91  
 ::: :||| :||| :||| :||| :||| :||| :|||  
 Db 208 GCGGTCAAGAACGGTGGCGT-----AGTGGCAGAACGGGCCACTTCGAAG 161  
 GENERAL INFORMATION:  
 Qy 92 LeuAsnArgLeuIleProPro-----SerSerArgGluArg 103  
 ||| :||| :||| :||| :||| :|||  
 Db 160 CTCACAGACCACTTCCACCGACTCTCACTCACTGCTCATCGCGTACGATC 101  
 ; Sequence 1, Application US/09214808A  
 ; Patent No. 6415793  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosenthal, Andre  
 ; APPLICANT: Freiberg, Christoph  
 ; APPLICANT: Perret, Xavier Philippe  
 ; APPLICANT: Broughton, William John  
 ; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic  
 ; Patent No. 6415793  
 ; TITLE OF INVENTION: Plasmid  
 ; FILE REFERENCE: CARP0068  
 ; CURRENT APPLICATION NUMBER: US/09/214, 808A  
 ; CURRENT FILING DATE: 1999-06-22  
 ; PRIORITY NUMBER: PCT/IB97/00950  
 ; PRIOR FILING DATE: 1997-07-10  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 1  
 ; LENGTH: 536165  
 ; TYPE: DNA  
 ; ORGANISM: Rhizobium  
 ; US-09-214-008-1

Alignment Scores:  
 Pred. No.: 1.07e+04  
 Score: 85.00  
 Percent Similarity: 37.50%  
 Best Local Similarity: 29.17%  
 Query Match: 13.80%  
 DB: 4  
 Gaps: 6

US-10-659-782A-32 (1-116) × US-09-214-808-1 (1-536165)

Qy 3 SerProGlyThrVal-CysSerLeuIleGlyMetLeuIleTrpLeuAspLeuAlaMe 22  
 ||| :||| :||| :||| :|||  
 Db 82810 GCCTCTGGATCGCTGCCTGCTGCGCTG---TTGCAC TGCGGCC 82775  
 ; ProHisValValProAlaLeuPr 51  
 ; :||| :||| :||| :|||  
 ; 82714 AGCCCTTCATGCTCTCGGCCGGAAACCGATCGCTCGGCCGATCGAGGCCGATCGCTGCC 82655  
 ; :||| :||| :|||  
 ; 82774 GGCTGATCAGCGGGTTCAAGACCTTCGACCTTGAAACCGTGGCTGCCGCCGCC 82715  
 ; :||| :||| :|||  
 ; 42 sAla-----  
 ; :||| :||| :|||  
 ; 82654 GCCCGTAACACGATCTGTCATCGCCGAGATGGCTGAGTCAG 82595  
 ; :||| :||| :|||  
 ; 66 -----AlaSerValPheSerIleSerThrLysAspSer-----GlySerAs 79  
 ; :||| :||| :|||  
 ; 82594 CGGTCAAGCGCCAGTGTGCTCGAGGGCAGCTGGATCCCTGTGTTAAAAGCTGCG 82535  
 ; :||| :||| :|||  
 ; 79 pLeuThrValSer-GlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProPro 99  
 ; :||| :||| :|||  
 ; 82534 GCTGACCTGGTCGATCTGACCGTGTGCTCATCCGCCAACGCCCTCGAGATAATGTCGCCCGT 82475  
 ; :||| :||| :|||  
 ; 99 erSerArgGluArgSerArgSerHisGlnProSer-----CysSerP 114  
 ; :||| :||| :|||  
 ; 82474 CTCCGATCTGTTGATCGGGCAAACGAAATCAGGCTCTCGAACCATTTGCTCGC 82415  
 ; :||| :||| :|||  
 ; 114 roGluIeu 116  
 ; :||| :|||  
 ; 82407 CGCGTC 82407  
 ; RESULT 10  
 ; US-09-252-991A-13395/C  
 ; Sequence 13395, Application US/0922991A

Alignment Scores:  
 Pred. No.: 1.82  
 Score: 87.00  
 Percent Similarity: 35.86%  
 Best Local Similarity: 28.28%  
 Query Match: 14.12%  
 DB: 2  
 Gaps: 8

US-10-659-782A-32 (1-116) × US-09-213-767-1 (1-2266)

Qy 2 ProSerProGlyThrValCysSerLeu-----LeuLeuGlyMetLeuTrpLeu 18  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 Db 797 CCTTCACCATCCAGTCAGTCAGCTGAGGCCACCCCTCACTCGGCCACTCTGCG---- 853  
 ; 19 AspLeuAlaMetAlaGlySerSerPheLeuSerPro--GluHisGlnArgVal 37  
 ; :||| :||| :||| :||| :|||  
 ; 854 -----TGTCCCCAAATGCACTCTGCACTGGCGAGCGAG 886  
 ; :||| :||| :||| :|||  
 ; 38 ArgProProHisLysAlaProHisValVal-----ProAlaLeuProLeu 52  
 ; :||| :||| :||| :|||  
 ; 887 CACCCCTTCGGGAGCAAGGACCACTCCAAAGCCCCCTGGAGGCCCTGAGCTG 946  
 ; :||| :||| :|||  
 ; 53 SerAsnGlnLeuCys----- 57  
 ; :||| :||| :|||  
 ; 947 AAGAGGCCGGCTTCGAGGTCACTCTGAGCCGAGGCCAACCTGAAAT 1006  
 ; :||| :||| :|||  
 ; 58 -----AspLeuGluIleGlnLysArgHistpRalaSerValPheSerGlnSerThrLysAsp 75  
 ; :||| :||| :||| :|||  
 ; 1007 CGAAGAGCTTAATGCGAGCCGGTTGGCCGGGTTGGAGAGCTGGAGCTG 1066  
 ; :||| :||| :|||  
 ; 76 SerGlySerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeu 95  
 ; :||| :||| :|||  
 ; 1067 AACGGC-----CCAAGGAAAGACTGGAAAGTCGGCCGGAAACGAAATCAGGCTCTCGAACCATTTGCTCGC 1171  
 ; :||| :||| :|||  
 ; 96 PhePro-----ProSerSerArgGluArgSerArgSerHisGlnProSer 111  
 ; :||| :||| :|||  
 ; 112 TGGCAGAAACCAAGGCCGAGCCAGAGTCCTCCACAGGGCGTGCAGGCCGCC 1171  
 ; :||| :||| :|||  
 ; 112 CysSerProGluIeu 116

Qy

Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196 136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: 1998-02-18  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO: 13395  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13395

Alignment Scores:  
Pred. No.: 1.53 Length: 867  
Score: 82.50 Matches: 28  
Percent Similarity: 48.65% Conservative: 8  
Best Local Similarity: 37.84% Mismatches: 28  
Query Match: 1.3.39% Indels: 11  
DB: 4 Gaps: 1

US-10-659-782a-32 (1-116) × US-09-252-991A-13395 (1-867)

Qy 47 ValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGluGlnArgHisTrpAla 66  
Db 638 GTCTCCAGCTTGCACCGCCAGTTCGGTGGCCACTTGCG 579

Qy 67 SerValPheSerGlnSer-----ThrlyBaspSerGly 77  
Db 578 ACCCTGGCAGTTGCCCTGGCCATGGCTCCGGTCAAGGGACCAAGAT 519

Qy 78 SerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPhePro 97  
Db 518 TGGACTTGATCGCAGTGGGACTGGTGGGGACTGGT-CTCAGCTCACAGGCGACAGGGCCA 460

Qy 98 -ProSerSerArgGluArgSerArgArgSerHisGlnPro 110  
Db 459 GCCGGGATCGCCTGAGGGCTTCCCACCGCA 420

RESULT 11  
US-09-252-991A-13604/c  
Sequence 133604, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196 136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US/09/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO: 13604  
LENGTH: 2103  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13604

Alignment Scores:  
Pred. No.: 5.7 Length: 2103  
Score: 82.50 Matches: 28  
Percent Similarity: 48.65% Conservative: 8  
Best Local Similarity: 37.84% Mismatches: 28  
Query Match: 13.39% Indels: 11

DB: 4 Gaps: 1  
Gaps: 1  
US-10-659-782a-32 (1-116) × US-09-252-991A-13604 (1-2103)  
Qy 47 ValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGluGlnArgHisTrpAla 66  
Db 471 GTCTCCAGCTTGCACCGCCAGTTCGGCCACTTGCGTGGCCACTTGCG 412  
67 SerValPheSerGlnSer-----ThrlyBaspSerGly 77  
Db 411 ACCCTGGCAGTTGCAGTTCGGTGGCCACTGGT-CTCAGCTCACAGGCGACAGGGCCA 352  
78 SerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPhePro 97  
Db 351 TCGGACTTGATCGCAGTGGCTGGCCACTGGT-CTCAGCTCACAGGCGACAGGGCCA 293  
98 -ProSerSerArgGluArgSerArgArgSerHisGlnPro 110  
Db 292 GCCGGGATCGCCTGCTGAGCACGGTTCACAGGCCA 253

RESULT 12  
US-09-252-991A-13746  
Sequence 13746, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196 136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US/09/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US/09/074,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO: 13746  
LENGTH: 3222  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13746

Alignment Scores:  
Pred. No.: 10.8 Length: 3222  
Score: 82.50 Matches: 28  
Percent Similarity: 48.65% Conservative: 8  
Best Local Similarity: 37.84% Mismatches: 28  
Query Match: 13.39% Indels: 11  
DB: 4 Gaps: 1

US-10-659-782a-32 (1-116) × US-09-252-991A-13746 (1-3222)  
Qy 47 ValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGluGlnArgHisTrpAla 66  
Db 2510 GTCTCCAGCTTGCACCGCCAGTTCGGCCACTTGCGTGGCCACTTGCG 2569  
67 SerValPheSerGlnSer-----ThrlyBaspSerGly 77  
Db 2570 ACCCTGGCAGTTGCAGTTCGGTGGCCACTGGT-CTCAGCTCACAGGCGACAGGGCCA 2629  
78 SerAspLeuThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPhePro 97  
Db 2630 TCGGACTTGATCGCAGTGGCTGGCCACTGGT-CTCAGCTCACAGGCGACAGGGCCA 2688  
98 -ProSerSerArgGluArgSerArgArgSerHisGlnPro 110  
Db 2689 GCCGGGATCGCCTGCTGAGCACGGTTCACAGGCCA 2728

RESULT 13  
US-09-976-255-2  
Sequence 2, Application US/08976255  
Patent No. 6136581  
GENERAL INFORMATION:

1 / APPLICANT: Jono, Keith E.  
 1 / TITLE OF INVENTION: KINASE GENES AND USES  
 1 / NUMBER OF SEQUENCES: 53 .  
 1 / ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071-2066  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FASTSEQ for Windows 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08-976,255  
 FILING DATE: NO. 6136581ember 21, 1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/031,675  
 FILING DATE: NO. 6136581ember 22, 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard J.  
 REGISTRATION NUMBER: 32,327  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5267 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-976-255-2

Alignment Scores:  
 Pred. No.: 29.5 Length: 5267  
 Score: 81.50 Matches: 37  
 Percent Similarity: 29.27% Conservative: 11  
 Best Local Similarity: 22.56% N mismatches: 53  
 Query Match: 13.23% Indels: 63  
 DB: 3 3 Gaps: 6

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Alignment Scores:  
 Pred. No.: 14 GlyMatLeuTrpLeuAspLeuAlaMetAlaGlySer-----SerPheLeu 28  
 Score: 4355 CGGCCTTTAGCTTGTCTGGCCATGGGCCACAGTCGCTGCTAC 4414  
 Percent Similarity: 14.00% Conservative: 11  
 Best Local Similarity: 13.00% N mismatches: 53  
 Query Match: 13.00% Indels: 63  
 DB: 3 3 Gaps: 6

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Alignment Scores:  
 Pred. No.: 29 SerProGluHisGlnArgValGlnValArgProProProHisLysAlaProHisValValPro 48  
 Score: 4415 ACACATACACTCAAAGGCCAGTGCCCTGGAACGGGCCACCCCTCCTAC 4474  
 Percent Similarity: 14.00% Conservative: 11  
 Best Local Similarity: 13.00% N mismatches: 53  
 Query Match: 13.00% Indels: 61  
 DB: 3 3 Gaps: 6

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Alignment Scores:  
 Pred. No.: 55 GlnArgLysSerGlySer-----GluGlnGlnArgHisTrpAlaSerVal 6082  
 Score: 6116 ACGGTGTGTGATCTTGTGGCTGGCCCATGGGGGACATGGCCCGGCTTCGCTGT 6135  
 Percent Similarity: 14.00% Conservative: 11  
 Best Local Similarity: 13.00% N mismatches: 53  
 Query Match: 13.00% Indels: 61  
 DB: 3 3 Gaps: 6

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Alignment Scores:  
 Pred. No.: 6082 ValGlnValArgProProHisLysAlaProHisValValProAlaLeuProLeuSerAsn 54  
 Score: 6017 CRCCCCAAAGCCAGGCCACACC-TGCACAAACCCAGGGCACAGGCCAGGGCTTCAGGA 6075  
 Percent Similarity: 14.00% Conservative: 12  
 Best Local Similarity: 13.00% N mismatches: 46  
 Query Match: 13.00% Indels: 36  
 DB: 4 4 Gaps: 4

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Alignment Scores:  
 Pred. No.: 1 MatProSerProGlySerGlySer-----LeuLeuLeuLeuGly 14  
 Score: 6017 CRCCCCAAAGCCAGGCCACACC-TGCACAAACCCAGGGCACAGGCCAGGGCTTCAGGA 6075  
 Percent Similarity: 14.00% Conservative: 12  
 Best Local Similarity: 13.00% N mismatches: 46  
 Query Match: 13.00% Indels: 36  
 DB: 4 4 Gaps: 4

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Alignment Scores:  
 Pred. No.: 15 MatLeuTrpLeuAspLeuAlaMetAlaGlySer 6076 CACCTG  
 Score: 6082 -----TGAGGTGTGCTGCTGGCTGGCCATGGCCCGGCTTCGCTGT 6135  
 Percent Similarity: 14.00% Conservative: 12  
 Best Local Similarity: 13.00% N mismatches: 46  
 Query Match: 13.00% Indels: 36  
 DB: 4 4 Gaps: 4

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Alignment Scores:  
 Pred. No.: 55 GlnLeuCysAspLeu-----GluGlnGlnArgHisTrpAlaSerVal 6082  
 Score: 6116 ACGGTGTGTGATCTTGTGGCTGGCCCATGGGGGACATGGCCCGGCTTCGCTGT 6135  
 Percent Similarity: 14.00% Conservative: 12  
 Best Local Similarity: 13.00% N mismatches: 46  
 Query Match: 13.00% Indels: 61  
 DB: 3 3 Gaps: 6

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Alignment Scores:  
 Pred. No.: 69 PheSerGlnSerThrLysAspSerGlySerAspLeuThrValSerGlyArgThrTrpGly 88  
 Score: 6116 GCGCCAACTATCGGAGATTCTGACCTGCTGGTGTGACCACTGACCCGGGG 6255  
 Percent Similarity: 14.00% Conservative: 12  
 Best Local Similarity: 13.00% N mismatches: 46  
 Query Match: 13.00% Indels: 61  
 DB: 3 3 Gaps: 6

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Alignment Scores:  
 Pred. No.: 89 LeuArgValLeuAsnArgLeuProProSerSerArg 89  
 Score: 6256 TTGACCCACTGACCCAGAGTCCTCCGGCAGGAACTTCCCGGCAAGAACTC 6315  
 Percent Similarity: 14.00% Conservative: 12  
 Best Local Similarity: 13.00% N mismatches: 46  
 Query Match: 13.00% Indels: 61  
 DB: 3 3 Gaps: 6

US-10-659-782A-32 (1-116) x US-08-976-255-2 (1-5267)

Alignment Scores:  
 Pred. No.: 106 ArgSerGlnProSerSerPro 114  
 Score: 6256 TTGACCCACTGACCCAGAGTCCTCCGGCAGGAACTTCCCGGCAAGAACTC 6315  
 Percent Similarity: 14.00% Conservative: 12  
 Best Local Similarity: 13.00% N mismatches: 46  
 Query Match: 13.00% Indels: 61  
 DB: 3 3 Gaps: 6



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 10, 2005, 14:15:44 ; Search time 467 Seconds (without alignment)

Perfect score: 1427.244 Million cell updates/sec

Title: US-10-659-782A-32

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4300275 seqs, 2072944193 residues

Total number of hits satisfying chosen parameters: 8600550

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Command line parameters:

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-Q:/cgn2_1/USPTO_spoof/US10659782/runat_05022005_161919_4325/app_query.fasta_1_263
-DB:/Published Applications NA -OFMT=fasta -SUFFIX=xlpb -MINMATCH=0.1
-LOOPCL=0 -LOOPCPE=0 -UNITS=8bits -START=1 -END=-1 -MATRIXX=blossom62
-TRANS=human0.cdi -LIST=45 -DOALIGN=00 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10659782 @runat_05022005_161919_4325
-NCPU=6 -ICU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100
-DLONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADD=1 -XGAPEXT=0.5
-YGAPOP=6 -YGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Database : Published Applications NA \*

- 1: /cgn2\_6/ptodata/2/pubna/US07\_PUBCOMB.seq;\*
- 2: /cgn2\_6/ptodata/2/pubna/PCT\_NW\_PUB.seq;\*
- 3: /cgn2\_6/ptodata/2/pubna/US06\_NW\_PUB.seq;\*
- 4: /cgn2\_6/ptodata/2/pubna/US05\_PUBCOMB.seq;\*
- 5: /cgn2\_6/ptodata/2/pubna/US07\_NW\_PUB.seq;\*
- 6: /cgn2\_6/ptodata/2/pubna/PECTUS\_PUBCOMB.seq;\*
- 7: /cgn2\_6/ptodata/2/pubna/US08\_NW\_PUB.seq;\*
- 8: /cgn2\_6/ptodata/2/pubna/US09\_PUBCOMB.seq;\*
- 9: /cgn2\_6/ptodata/2/pubna/US09B\_PUBCOMB.seq;\*
- 10: /cgn2\_6/ptodata/2/pubna/US09B\_PUBCOMB.seq;\*
- 11: /cgn2\_6/ptodata/2/pubna/US09C\_PUBCOMB.seq;\*
- 12: /cgn2\_6/ptodata/2/pubna/US09\_NW\_PUB.seq;\*
- 13: /cgn2\_6/ptodata/2/pubna/US10A\_PUBCOMB.seq;\*
- 14: /cgn2\_6/ptodata/2/pubna/US10B\_PUBCOMB.seq;\*
- 15: /cgn2\_6/ptodata/2/pubna/US10C\_PUBCOMB.seq;\*
- 16: /cgn2\_6/ptodata/2/pubna/US10D\_PUBCOMB.seq;\*
- 17: /cgn2\_6/ptodata/2/pubna/US10E\_PUBCOMB.seq;\*
- 18: /cgn2\_6/ptodata/2/pubna/US10I\_NW\_PUB.seq;\*
- 19: /cgn2\_6/ptodata/2/pubna/US11\_NW\_PUB.seq;\*
- 20: /cgn2\_6/ptodata/2/pubna/US60\_NW\_PUB.seq;\*
- 21: /cgn2\_6/ptodata/2/pubna/US60\_PUBCOMB.seq;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	220	35.7	447	15	US-10-659-191A-11
2	214	34.7	351	9	US-09-794-987-1
3	214	34.7	351	12	US-09-796-158-1
4	214	34.7	351	15	US-10-86-414-3
5	214	34.7	351	15	US-10-86-706-1
6	214	34.7	351	18	US-10-679-813-1
7	214	34.7	401	17	US-10-477-506-3
8	214	34.7	510	17	US-10-477-506-4
9	214	34.7	511	15	US-10-191-997-112
10	214	34.7	527	9	US-09-833-253-1
11	214	34.7	596	13	US-10-098-841-252
12	214	34.7	654	9	US-09-989-722-267
13	214	34.7	654	9	US-09-989-723-267
14	214	34.7	654	9	US-09-989-279-67
15	214	34.7	654	9	US-09-989-721-67
16	214	34.7	654	9	US-09-989-731-67
17	214	34.7	654	9	US-09-989-732-67
18	214	34.7	654	9	US-09-991-073-267
19	214	34.7	654	9	US-09-990-442-267
20	214	34.7	654	9	US-09-991-163-67
21	214	34.7	654	9	US-09-993-604-267
22	214	34.7	654	9	US-09-990-456-267
23	214	34.7	654	9	US-09-993-598-267
24	214	34.7	654	9	US-09-990-436-267
25	214	34.7	654	9	US-09-989-293A-267
26	214	34.7	654	9	US-09-989-735-67
27	214	34.7	654	9	US-09-990-444-267
28	214	34.7	654	9	US-09-991-181-267
29	214	34.7	654	9	US-09-989-730-67
30	214	34.7	654	9	US-09-990-436-267
31	214	34.7	654	9	US-09-993-687-267
32	214	34.7	654	10	US-09-989-734-267
33	214	34.7	654	10	US-09-987-633-267
34	214	34.7	654	10	US-09-989-724-267
35	214	34.7	654	10	US-09-989-728-267
36	214	34.7	654	10	US-09-990-441-267
37	214	34.7	654	10	US-09-993-687-267
38	214	34.7	654	10	US-09-997-656-267
39	214	34.7	654	10	US-09-990-418-267
40	214	34.7	654	10	US-09-990-562-267
41	214	34.7	654	10	US-09-990-711-267
42	214	34.7	654	10	US-09-989-776-267
43	214	34.7	654	10	US-09-989-156-267
44	214	34.7	654	10	US-09-998-156-267
45	214	34.7	654	10	US-09-990-437-267

## ALIGNMENTS

RESULT 1  
US-10-294-191A-11  
Sequence 11, Application US/10294191A  
Publication No. US20030211512A1  
GENERAL INFORMATION:  
/ APPLICANT: Rothschild, Max F.  
/ APPLICANT: Kim, Kwan Suk  
/ APPLICANT: Anderson, Lloyd L.  
TITLE OF INVENTION: Novel Ghrelin Alleles and Use of the Same for Genetically Typing  
FILE REFERENCE: P05408051  
CURRENT APPLICATION NUMBER: US/10/294,191A  
CURRENT FILING DATE: 2002-11-14  
PRIORITY APPLICATION NUMBER: US 60/333,222  
PRIORITY FILING DATE: 2001-11-14  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 11  
LENGTH: 447  
TYPE: DNA  
ORGANISM: Porcine  
US-10-294-191A-11

## SUMMARIES

Alignment Scores:  
 Pred. No.: 3.29e-18 Length: 447  
 Score: 220.00 Matches: 65  
 Percent Similarity: 57.81% Conservative: 9  
 Best Local Similarity: 50.78% Mismatches: 36  
 Query Match: 35.71% Indels: 18  
 DB: 15 Gaps: 5

US-10-659-782A-32 (1-116) x US-10-294-191A-11 (1-447)

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeutTrpLeu---Asp 19  
 Db 11 ATGCCCTCACGGGACATTGACCTGCTGTCTCATGGCAGAC 70

Qy 20 LeuAlaMetAlaGly1SerSerProGluHiSerGlnArgValGlnValArgPro 39  
 Db 71 TGGCCATGGGGCTTCAGCTTCTGAGCCCGAACACCAAGAAAGTGCAGGTAAAGCT 130

Qy 40 ProHisLysAlaPro---HisValValProAlaLeuProLeuSerAsnGin 55  
 Db 131 CTCCCCAGAGCCCCGCTCTGGGGRACTCATCAGGCCCTCAGTTGGACC 190

Qy 56 LeuCysAspLeuGluGlnGlnArgHiSerAlaSerAlaSerAla1PheSerGlnSer-  
 Db 191 TGGGCTCACCTG-----cTCGGCTCTGGCTCTCCCAAGGGAGACTCTGG 238

Qy 75 SP---SerglySerAspLeuThrVal-----SerglyArgHiTrpG 88  
 Db 239 ATCTGAAAGGGGCCATACCTTGCTGCTCTGGAAAGGAAGTAGTGGGGTGGTGGG 298

Qy 88 LysLeuArgValLeuAsnArgLeuPheProProSerSerArgGluArgSerH 108  
 Db 299 CATCTAGGGCTCAAGAGGAGTCTCTTCCAGAGAAGGATCAAGAGCC 358

Qy 108 isGlnProSerCysSerPro 114  
 Db 359 ACCAGCCAACCTGAAGCCC 378

RESULT 2  
 US-09-794-987-1  
 Sequence 1, Application US/09794987  
 Patent No. US200401791A1  
 GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 Deisher, Theresa A.  
 TITLE OF INVENTION: MOTILIN HOMOLOGS  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue, East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102

COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ For Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/794,987  
 FILING DATE: 27-Feb-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sawislak, Deborah A.  
 REGISTRATION NUMBER: 37,438  
 REFERENCE/DOCKET NUMBER: 97-04  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-442-6672

RESULT 3  
 US-09-796-158-1  
 Sequence 1, Application US/09796158  
 Publication No. US2004025445A1  
 GENERAL INFORMATION:  
 APPLICANT: Sheppard, Paul O.  
 Deisher, Theresa A.  
 TITLE OF INVENTION: MOTILIN HOMOLOGS  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue, East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ For Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/794,987  
 FILING DATE: 27-Feb-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sawislak, Deborah A.  
 REGISTRATION NUMBER: 37,438  
 REFERENCE/DOCKET NUMBER: 97-04  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-442-6672

TELEFAX: 206-442-6678  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 351 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: sig\_peptide  
 LOCATION: 1..351  
 OTHER INFORMATION: SEQ ID NO: 1 :  
 US-09-794-987-1

Alignment Scores:  
 Pred. No.: 1.39e-17 Length: 351  
 Score: 214.00 Matches: 51  
 Percent Similarity: 44.48% Conservative: 1  
 Best Local Similarity: 43.53% Mismatches: 0  
 Query Match: 34.74% Indels: 65  
 DB: 9 Gaps: 1

US-10-659-782A-32 (1-116) x US-09-794-987-1 (1-351)

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeutTrpLeuAspLeu 20  
 Db 1 ATGCCCTCCAGGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGACTGGACTTG 60

Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHiSerGlnArgValGlnValArgProPro 40  
 Db 61 GCCATGGCAGCCCTCAGCTCTGGCCCTGAACCCGAGAGTCAG----- 108

Qy 41 HisLysAlaProHisValValProLeuSerAsnGlnLeuCysAspLeuGlu 60  
 Db 108 ----- 108

Qy 61 GlnGlnArgHistidylPheSerGlnSerThrLysAspSerGlySerAspLeu 80  
 Db 108 ----- 108

Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSer 100  
 Db 108 ----- 108

Qy 101 Arg-Glu-LysArgSerArgSerHisGlnProSerCysSerProGluLeu 116  
 Db 109 CAGAGAAAGGAGTCGAAGAGCCAGCCAAAGCTGAGCCGGGAGCTC 157



PRIOR APPLICATION NUMBER: 60/041,102  
 PRIOR FILING DATE: 1997-03-24  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 1  
 LENGTH: 351  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1) . . . (351)

Alignment Scores:  
 Pred. No.: 1 1.39e-17 Length: 351  
 Score: 214.00 Matches: 51  
 Percent Similarity: 44.44% Conservative: 1  
 Best Local Similarity: 43.59% Mismatches: 0  
 Query Match: 34.74% Indels: 65  
 DB: 18 Gaps: 1

US-10-659-782a-32 (1-116) x US-10-679-813-1 (1-351)

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20  
 Db 1 ATGCCCTCCCAAGCCGACCCCTCTGCAGCCCTCGCATGCTCGCTGACTTG 60

Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluIleGlnArgValGlnValArgProPro 40  
 Db 61 GCCATGGCAGGGCTCAGCTTCCAGCTGAACCAGAGTCAG----- 108

Qy 41 HisLysAlaProHisValValProLeuSerAsnGlnLeuCysAspLeuGlu 60  
 Db 108 ----- 108

US-10-659-782a-32 (1-116) x US-10-607-706-1 (1-351)

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20  
 Db 1 ATGCCCTCCCAAGCCGACCCCTCTGCAGCCCTCGCATGCTCGCTGACTTG 60

Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluIleGlnArgValGlnValArgProPro 40  
 Db 61 GCCATGGCAGGGCTCAGCTTCCAGCTGAACCAGAGTCAG----- 108

Qy 41 HisLysAlaProHisValValProLeuSerAsnGlnLeuCysAspLeuGlu 60  
 Db 108 ----- 108

Qy 61 GlnGlnArgHistRpaSerValPheSerGlnSerThrLysAspSerAspLeu 80  
 Db 108 ----- 108

Qy 81 ThrValSerGlyArgThrRpGlyLeuArgValueAsnArgLeuPheProProSer 100  
 Db 108 ----- 108

Qy 101 Arg-GluArgSerArgSerHisGlnProSerCysSerProGluLeu 116  
 Db 109 CAGAGAAAGGAGTCGAGAAGCCACAGCCAAAGCTGAGCCCCAGCTC 157

RESULT 7  
 US-10-477-506-3  
 Sequence 3, Application US/10477506  
 ; Publication No. US20040157227A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chopin, Lisa K.  
 ; ATTORNEY/AGENT: Jeffery, Penelope L.  
 ; APPLICANT: Herington, Adrian C.  
 ; TITLE OF INVENTION: REPRODUCTIVE CANCER DIAGNOSIS AND THERAPY  
 ; FILE REFERENCE: 225181  
 ; CURRENT APPLICATION NUMBER: US/10/477,506  
 ; PRIORITY: 2003-11-10  
 ; PRIORITY NUMBER: PR9267  
 ; PRIORITY FILING DATE: 2003-11-10  
 ; PRIORITY NUMBER: PR4919  
 ; PRIORITY FILING DATE: 2001-05-10  
 ; PRIORITY NUMBER: PCT/AU02/000582  
 ; PRIORITY FILING DATE: 2002-05-10  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 3  
 ; LENGTH: 401  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

US-10-477-506-3

Alignment Scores:  
 Pred. No.: 1 1.64e-17 Length: 401  
 Score: 214.00 Matches: 51  
 Percent Similarity: 44.44% Conservative: 1  
 Best Local Similarity: 43.59% Mismatches: 0  
 Query Match: 34.74% Indels: 65  
 DB: 17 Gaps: 1

US-10-659-782a-32 (1-116) x US-10-477-506-3 (1-401)

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTrpLeuAspLeu 20  
 ;  
 NAME/KEY: CDS  
 LOCATION: (1) . . . (351)  
 US-10-679-813-1

Db 33 ATGCCCTCCCGGACCGTGCACCCCTGGCATGGCTGGACTTG 92  
 Qy 21 AlaMetAlaGlySerSerpheLeuSerProGluHisGlnArgValGlnValArgProPro 40  
 Db 93 GCCATCGCAAGCTCCAGCTTCAGCTTCAGCCCTGAAACCCAGAGTCAG----- 140  
 Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60  
 Db 140 ----- 140  
 Qy 61 GlnGinArgHistRPLasSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80  
 Db 140 ----- 140  
 Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100  
 Db 140 ----- 140  
 Qy 101 Arg-GluarSerArgArgSerHisGlnProSerCysSerProGluLeu 116  
 Db 141 CAGAGAAAGGTCCAGCTCAGGCCAACGCCCCGAGCTC 189  
 RESULT 9  
 US-10-191-997-112  
 ; Sequence 112, Application US/10191997  
 ; Publication No. US20030207334A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Oligos Etc., Inc.  
 ; APPLICANT: DALE, Roderic M. K.  
 ; APPLICANT: ARROW, Amy  
 ; APPLICANT: THOMPSON, Terry  
 ; TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their  
 ; FILE REFERENCE: 54800-5019  
 ; CURRENT APPLICATION NUMBER: US/10/191,997  
 ; CURRENT FILING DATE: 2003-07-10  
 ; PRIORITY APPLICATION NUMBER: US 60/303,820  
 ; PRIORITY FILING DATE: 2001-07-10  
 ; NUMBER OF SEQ ID NOS: 132  
 ; SEQ ID NO: 112  
 ; LENGTH: 511  
 ; TYPE: DNA  
 ; ORGANISM: HOMO sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: NM\_016362  
 US-10-191-997-112  
 Alignment Scores:  
 Pred. No.: 2.2e-17 Length: 511  
 Score: 214.00 Matches: 51  
 Percent Similarity: 44.44% Conservative: 1  
 Best Local Similarity: 43.5% Mismatches: 0  
 Query Match: 34.7% Indels: 65  
 DB: 15 Gaps: 1  
 US-10-659-782A-32 (1-116) x US-10-191-997-112 (1-511)  
 Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTriLeuAspLeu 20  
 Db 34 ATGCCTCCCGAACGGACCCTGACGCCCTGCTGCTGCTGCTGACTTG 93  
 Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40  
 Db 94 GCCATGCAAGCTTCAGCTTCAGCTTCAGCTTCAGCTGCTGCTGCTGACTTG 93  
 Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerGlnLeuCysAspLeuGlu 60  
 Db 141 ----- 141  
 Qy 61 GlnGinArgHistRPLasSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80  
 Db 141 ----- 141  
 Qy 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100  
 Db 141 ----- 141  
 Qy 101 Arg-GluarSerArgArgSerHisGlnProSerCysSerProGluLeu 116  
 Db 142 CAGAGAAAGGTCCAGCTCAGGCCAACGCCCCGGAGCTC 190  
 RESULT 10  
 US-09-853-253-1  
 ; Sequence 1, Application US/09853253  
 ; Patent No. US 20030055156A1

GENERAL INFORMATION:

APPLICANT: JASPERS, STEPHEN  
 APPLICANT: SHEPPARD, PAUL  
 APPLICANT: DEISHER, THEREZA  
 TITLE OF INVENTION: Zbig33-like Peptides  
 FILE REFERENCE: 00-30  
 CURRENT APPLICATION NUMBER: US/09/853,253  
 CURRENT FILING DATE: 2001-05-10  
 PRIOR APPLICATION NUMBER: 60/203,300  
 PRIOR FILING DATE: 2000-05-11  
 NUMBER OF SEQ ID NOS: 28  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 1  
 LENGTH: 527

TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE: CDS  
 NAME/KEY: CDS  
 LOCATION: (50) . . . (400)  
 US-09-853-253-1

Alignment Scores:

Pred. No.	Score:	Length:	Matches:	Mismatches:	Indels:	Gaps:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
2.28e-17	214.00	527	51	0	65	1	44.44%	43.59%	US-10-098-841-252	
2.28e-17	34.74%	527	51	0	65	1	44.44%	43.59%	US-10-098-841-252	

Length: 527  
 Matches: 51  
 Mismatches: 0  
 Indels: 65  
 Gaps: 1  
 Percent Similarity: 44.44%  
 Best Local Similarity: 43.59%  
 Query Match: 34.74%

US-10-659-782A-32 (1-116) × US-09-853-253-1 (1-527)

Qy 1 MetProSerProGlyThrValCysSerIleLeuGlyMetLeuTrpLeuAspIeu 20  
 Db 50 ATGCCCTCCAGGGACCGTGTGCACCTCTGCTCGCATGCTGGACTTG 109

Qy 21 AlaMetAlaGlySerSerPhenSerProGluHisGlnArgValGlnValArgProPro 40  
 Db 110 GCCATGCGAGCTCCAGCTTCAGCTTCAGCTGAGCCAAACCCCCGAGTCAG---- 157

Qy 41 HisLysAlaProHisValValProAlaLysProLeuSerAsnGlnLeuCysAspIeuGlu 60  
 Db 157 ----- 157

Qy 61 GlnGlnArgHistDpAlaSerValPheSerGlySerAspIeu 80  
 Db 157 ----- 157

Qy 81 ThrValSerGlyArgThrTpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100  
 Db 157 ----- 157

Qy 101 Arg-GluuArgSerArgSerHisGlnProSerCysSerProGluLeu 116  
 Db 158 CAGAGAAGGAGTCAAGAACGCCACAGGCAAGGCTCAGGCCGGAGCTC 206

RESULT 11  
 US-10-098-841-252  
 Publication No. US20020197679A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom  
 APPLICANT: Liu, Chenghua  
 APPLICANT: Asundi, Vinod  
 APPLICANT: Xu, Chongjun  
 APPLICANT: Zhou, Ping  
 APPLICANT: Ma, Yunqing  
 APPLICANT: Wang, Jian-Rui  
 APPLICANT: Zhao, Qing A.  
 APPLICANT: Ren, Feiyuan  
 APPLICANT: Chen, Rui-hong  
 APPLICANT: Wang, Dunrui  
 APPLICANT: Wang, Zhiwei

APPLICANT: Wehrman, Tom  
 APPLICANT: Zhang, Jie  
 APPLICANT: Qian, Xiaohong B.  
 APPLICANT: Dirmancic, Radope T.  
 TITLE OF INVENTION: No. US20020197679A1 Nucleic Acids and Polypeptides  
 FILE REFERENCE: 784CIP2  
 CURRENT APPLICATION NUMBER: US/10/098,841  
 CURRENT FILING DATE: 2002-03-13  
 PRIOR APPLICATION NUMBER: 09/538,012  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: 09/552,317  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: 09/488,725  
 PRIOR FILING DATE: 2000-01-21  
 NUMBER OF SEQ ID NOS: 331  
 SOFTWARE: Pt\_Fl\_genes Version 1.0  
 SEQ ID NO: 252  
 LENGTH: 596  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE: CDS  
 NAME/KEY: CDS  
 LOCATION: (111) . . . (464)  
 US-10-098-841-252

Alignment Scores:

Pred. No.	Score:	Length:	Matches:	Mismatches:	Indels:	Gaps:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
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2.65e-17	34.74%	596	51	0	65	1	44.44%	43.59%	US-10-098-841-252	

Length: 596  
 Matches: 51  
 Mismatches: 0  
 Indels: 65  
 Gaps: 1  
 Percent Similarity: 44.44%  
 Best Local Similarity: 43.59%  
 Query Match: 34.74%

US-10-659-782A-32 (1-116) × US-10-098-841-252 (1-596)

Qy 1 MetProSerProGlyThrValCysSerIleLeuGlyMetLeuTrpLeuAspIeu 20  
 Db 111 ATGCCCTCCAGGGACCGTGTGCACCTCTGCTCCCTCGCATCTCTCGCTGGACTTG 170

Qy 21 AlaMetAlaGlySerSerPhenSerProGluHisGlnArgValGlnValArgProPro 40  
 Db 171 GCCATGCGAGGCTCCAGCTTCAGCTGAGCCCTGAACCCAGAGTCAG----- 218

Qy 41 HisLysAlaProHisValValProAlaLysProLeuSerAsnGlnLeuCysAspIeuGlu 60  
 Db 41 HisLysAlaProHisValValProAlaLysProLeuSerAsnGlnLeuCysAspIeuGlu 60

Db 218 ----- 218

Qy 61 GlnGlnArgHistDpAlaSerValPheSerGlySerAspIeu 80  
 Db 61 GlnGlnArgHistDpAlaSerValPheSerGlySerAspIeu 80

Db 218 ----- 218

Qy 81 ThrValSerGlyArgThrTpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100  
 Db 218 ----- 218

Qy 101 Arg-GluuArgSerArgSerHisGlnProSerCysSerProGluLeu 116  
 Db 219 CAGAGAAGGAGTCAAGAACGCCACAGGCAAGGCTCAGGCCGGAGCTC 267

RESULT 12  
 US-09-989-722-267  
 Sequence 267, Application US/09989722  
 GENERAL INFORMATION:  
 Patent No. US20020197679A1  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Bottstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Kijavin, Ivar J.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin X.  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2730PI053  
 CURRENT APPLICATION NUMBER: US/09/989,722  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Alignment Scores:
Pred. No.: 2.97e-17 Length: 654
Score: 214.00 Matches: 51
Percent. Similarity: 44.44% Conservative: 1
Best Local Similarity: 43.59% Mismatches: 0
Query Match: 34.74% Indels: 65
DB: 9 Gaps: 1

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Db 176 ATGCCCTCCAGGACCGTGTGAGCCCTCTGAGCTCCTGGCATGCTGGTGGACTTG 235  
 Qy 21 AlamerAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40  
 Db 236 GCCATGCAGGTCAGCTTCCTGAGCTGAACCAACAGAGTCAG----- 283  
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 Db 283 ----- 283  
 Qy 61 GinGlnArgHistrpAlaSerValPheSerGlySerAspLeu 80  
 Db 283 ----- 283  
 Qy 101 Arg-GluArgSerArgSerArgSerHisGlnProSerCysSerProGluLeu 116  
 Qy 81 ThrValSerGlyArgThrPrglyLeuArgValLeuAsnArgLeuPheProProSerSer 100  
 Db 283 ----- 283  
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RESUME 14  
 US-09-989-279-267  
 / Sequence 267, Application US/09899279  
 / Patent No. 720020072496A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Ashkenazi, Avi J.  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Desnoyers, Luc  
 / APPLICANT: Eaton, Dan L.  
 / APPLICANT: Ferrara, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gerber, Hanspeter  
 / APPLICANT: Gerritsen, Mary E.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, J. Christopher  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Kijaviv, Ivar J.  
 / APPLICANT: Napier, Mary A.  
 / APPLICANT: Pan, James  
 / APPLICANT: Paon, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Watanabe, Colin K.  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William I.  
 / APPLICANT: Zhang, Zemin  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 / TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P27301PC56  
 CURRENT APPLICATION NUMBER: US/09/989,279  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/049,787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-06-17 ; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17 ; PRIOR APPLICATION NUMBER: 60/089801
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; PRIOR APPLICATION NUMBER: 60/091633 ; PRIOR FILING DATE: 1998-07-02

; Alignment Scores:
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; Query Match: 34.74% Indels: 65
; Db: 9 Caps: 1

US-10-659-782A-32 (1-116) x US-09-989-279-267 (1-654)

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Qy 41 HisLysAlaProHisValValProAlaLeuProLeuSerArgGlnLeuCysAspLeuGlu 60
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RESULT 15
US-09-989-727-267
; Sequence 267, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerbitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Klijavin, Ivar J.
; APPLICANT: Napiier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC65

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CURRENT APPLICATION NUMBER: US/09/989,727  
CURRENT FILING DATE: 2001-11-19  
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PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
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PRIOR APPLICATION NUMBER: 60/091360  
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PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

### **Alignment Scores:**

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Percent Local Similarity:	43.59%	Conservative:	1
Query Match:	34.74%	Mismatches:	0
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6-10-650 7821 22 (116) 2 000 707 267 1/ 2

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y	101	Arg-Glu-LysSerGlyArgSerHisGlnProSerCysSerProGluLeu	116
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ob time : 472 secs

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C	9	AY413165	30.8	542	4	AY413165	AY413165 Mus musculus	
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							AUTHORS	Dias Neto,E., da Silva,W. Jr., Correia,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Harte,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
							TITLE	TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
							JOURNAL	JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
							PUBMED	PUBMED 20203613
							COMMENT	COMMENT Contact: Simpson A.J.G.
								Laboratory of Cancer Genetics
								Ludwig Institute for Cancer Research
								Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
								Tel: +55-11-2704922
								Fax: +55-11-2707001
								Email: asimpson@ludwig.org.br
								This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

FEATURES	Source
(http://www.ludwig.org.br/scripts/gethtml12.pl?r1=CM2&r2=CM2-NT0185 071200-886-a07&t3=2000-12-07&t4=1)	
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Site_2: SmaI; A mini-library was made by cloning products	
derived from ORESTES PCR (U.S. Letters Patent application	
No. 196 716 - Ludwig Institute for Cancer Research)	
profiles into the PUC 18 vector. Reverse transcription of	
tissue mRNA and cDNA amplification were performed under	
low stringency conditions."	

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Dy	95 LeuPheProProSerSerArgLysArgSerIleArgSerIleGlnProSerCysSerPro	114			
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ACCESSION	AY413163				
VERSION	AY413163.1	GI:39769128			
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ORGANISM	Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrini; Homiridae; Homo.					
1 (bases 1 to 354)					
REFERENCE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Torenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.J., Periera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
AUTHORS	Inferring nonneutral evolution from human-Chimp-mouse orthologous				

JOURNAL	Science trios	302 (5652), 1960-1963 (2003)
PUBLISHED	14671302	
REFERENCE	2 (bases 1 to 354)	
AUTHORS	Clark, A.G., Gianoukakis, S., Nielson, R., Todd, M.A., Tzenenbaum, D.M., Civello, D., Ferriera, S., Wang, G., Zheng, X.H., Wh Adams, M.D. and Cargill, M.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-NOV-2003) Celera Genom Rockville, MD 20850, USA	
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Percent Similarity:	44.44%	Percent Similarity:	44.44%	Mismatches:	1																		
Best Local Similarity:	43.59%	Query Match:	34.74%	Indels:	0																		
DB:	9	DB:	1	Gaps:	65																		
US-10-659-782A-32 (1-116) x AY413163 (1-354)																							
Qy	1 Met Pro Ser Pro Gly Thr Val Cys Ser Ile Leu Ile Gln Met Leu Tyr Phe Leu Asp Leu 20	Db	1 ATGCCTCCCGGACGGTCAGCTCTCCCTGGATGCTCTGGCTGAATGCTGCTGGCTGAATGCTG 60	Qy	21 Ala Met Ala Gly Ser Ser Pro Heleu Ser Pro Glu His Gln Arg Val Gln Val Arg Pro Pro 40	Db	61 GCAATGGAGGTCTCAGTTCCTGAGCCCTGAAACACCGAGAGTCCAG 108	Qy	41 His Iys Ala Pro His Val Val Pro Ala Leu Pro Leu Ser Asn Gln Leu Cys Asp Leu Glu 60	Db	108 ----- 108	Qy	61 Glu Ile Arg His Ile Trp Ala Ser Val Phe Ser Gln Ser Thr Lys Asp Ser Gly Ser Asp Leu 80	Db	108 ----- 108	Qy	81 Thr Val Ser Gly Arg Thr Ile Phe Val Leu Ile Asn Arg Leu Ile Phe Pro Pro Ser Ser 100	Db	108 ----- 108	Qy	101 Arg Glu Arg Ser Arg Arg Ser His Gln Pro Ser Cys Ser Pro Glu Ile 116	Db	109 CAGGAAACGAGTGAAAGAGGCCAACGCAAAGCTGAGCCCCAGGCTC 157

JOURNAL	Unpublished (2002)	LOCUS	BM982194	bp	672	mRNA	linear	EST 21-FEB-2003
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4403 Email: yongsung@mail.kribb.re.kr Plate: yongsung@mail.kribb.re.kr 37 row: H column: 03 High quality sequence stop: 526.	DEFINITION	UI-CP-EN1-acr-k-05-0-UI-51	UI	CF-EN1	Homo sapiens	cDNA clone	
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FEATURES	source	AUTHORS	Bonaldo, M. P., Lennon, G. and Soares, M.B.					
FEATURES	source	TITLE	Normalization and subtraction: two approaches to facilitate gene discovery					
FEATURES	source	JOURNAL	Genome Res. 6 (9), 791-806 (1996)					
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FEATURES	source	/dev_stage="Adult"	/dev_stage="Adult"					
FEATURES	source	/lab_host="DH10B (Life Technologies)"	/lab_host="DH10B (Life Technologies)"					
FEATURES	source	/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI I; Site 2: Not I; UI-CP-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoRI I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (dR)18 tail. The sequence tag for this library is CTGTCAGCT. TAG TISSUE:Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h TAG LIB:UI-CP-EN1 TAG SEQ:CTGTCAGCT						
ORIGIN	Qy	Alignment Scores:	1.13e-11	Length:	526	Matches:	51	Score: 214.00
ORIGIN	Qy	Pred. No.:	2.14.00	Percent Conservative:	0	Indels:	65	Pred. No.: 51
ORIGIN	Qy	Score:		Niservatives:		Gaps:		Score: 44.44%
ORIGIN	Qy	Percent Similarity:	44.44%	Query Match:	34.74%	DB:	4	Percent Similarity: 44.44%
ORIGIN	Qy	Best Local Similarity:	43.59%	DB:	1	DB:	1	Best Local Similarity: 43.59%
ORIGIN	Qy	Query Match:	34.74%	DB:	4	DB:	1	Query Match: 34.74%
ORIGIN	Qy	DB:	1	DB:	1	DB:	1	DB: 1
ORIGIN	Qy	US-10-659-782A-32 (1-116) × BM854032 (1-526)						
ORIGIN	Qy	1 Met Pro Ser Pro Gly Arg Thr Val Cys Ser Leu Ile Leu Glu Asn Arg Leu Ile Triplet Asp Leu 20						
ORIGIN	Db	50 ATGCCCTCCAGGGACCTCGTCAGCTCCCTCGCATGCTGGATCTGGCTGACTTG 109						
ORIGIN	Qy	21 Ala Met Ala Gly Ser Ser Phe Leu Ser Pro Glu His Glu Arg Val Gln Val Arg Pro Pro 40						
ORIGIN	Db	110 GCGATGCCAGGTCCACCTTCTGAGCCCTGAACCAAGAGTCCTCCAG 157						
ORIGIN	Qy	41 His Lys Ala Pro His Val Val Pro Ala Leu Pro Leu Ser Asn Glu Leu Cys Asp Leu Glu 60						
ORIGIN	Db	157 ----- 157						
ORIGIN	Qy	61 Glu Glu Arg His Trp Ala Ser Val Phe Ser Val Phe Ser Val Phe Pro Pro Ser Ser 80						
ORIGIN	Db	157 ----- 157						
ORIGIN	Qy	81 Thr Val Ser Gly Arg Thr Trp Gly Leu Arg Val Leu Asn Arg Leu Phe Pro Pro Ser Ser 100						
ORIGIN	Db	157 ----- 157						
RESULT	Qy	101 Arg-Glu Arg Ser Arg Ser His Gln Pro Ser Cys Ser Pro Glu Leu 116						
RESULT	Db	158 CAGAGAAAGTCGAAAGCCACCAGGCCAGCTGAGCCCGAGCTC 206						

sequence that is located between the Not I site and the (dri)18 tail. The sequence tag for this library is ACATGAC.

TAG TISSUE=chondrosarcoma  
TAG\_LIB=UI-H-EI1  
TAG\_SEQ=ACATIGCAC"

ORIGIN

Alignment Scores:  
 Pred. No.: 1\_6e-11 Length: 678  
 Score: 214.00 Matches: 51  
 Percent Similarity: 44.44% Conservative: 1  
 Best Local Similarity: 43.59% Mismatches: 0  
 Query Match: 34.74% Indels: 65  
 Db: 6 Gaps: 1

US-10-659-782A-32 (1-116) x CA449820 (1-678)

Qy 81 ThrvalSerGlyArgThrTrpGlyLeuArgValLeuasnArgLeuPheProSerSer 100  
 Db 389 ----- 389

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116  
 Db 388 CAGAGAAGGAGTCGAGAACGCCAACGGCAAGCTGAAGCCCGAGCTC 340

RESULT 5

CA449820/c LCUS 678 bp mRNA linear EST 08-NOV-2002  
 DEFINITION UT-H-EII-ayy-c-12-0-UI-81 NCI CGAP EI1 Homo sapiens cDNA clone  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ORGANISM Homo sapiens (human)

ACCESSION CA449820 1 GI:24814240  
 VERSION EST.  
 KEYWORDS SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE NCI-NCAP http://www.ncbi.nlm.nih.gov/ncicb/gp.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 TITLE Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgsbps-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercende  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@uiowa.edu  
 Seq primer: M13 FORWARD  
 POLY=A:Yes

JOURNAL COMMENT

FEATURES Source  
 location/Qualifiers  
 1..678  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="rRNA"  
 /clone="UI-H-EII-ayy-c-12-0-UI"  
 /tissue\_type="Chondrosarcoma"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI CGAP EI1"  
 /note="Organ: Left Palvis; Vector: pT7T3-Pac (Pharmacia)  
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I.  
 NCI CGAP EI1 is a normalized cDNA library containing the  
 following tissue(s): Chondrosarcoma. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an EcoR I  
 adaptor, digested with Not I, and cloned directionally  
 into pT7T3-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the (dri)18 tail. The sequence tag for this library is ACATGAC.

TAG TISSUE=chondrosarcoma  
TAG\_LIB=UI-H-EI1  
TAG\_SEQ=ACATIGCAC"

ORIGIN

Alignment Scores:  
 Pred. No.: 1\_6e-11 Length: 678  
 Score: 214.00 Matches: 51  
 Percent Similarity: 44.44% Conservative: 1  
 Best Local Similarity: 43.59% Mismatches: 0  
 Query Match: 34.74% Indels: 65  
 Db: 6 Gaps: 1

US-10-659-782A-32 (1-116) x CA449820 (1-678)

Qy 81 ThrvalSerGlyArgThrTrpGlyLeuArgValLeuasnArgLeuPheProSerSer 100  
 Db 389 ----- 389

Qy 61 GlnGlnArgHistrpAlaserValPheSerGlySerAspLeu 80  
 Db 389 ----- 389

Qy 81 ThrvalSerGlyArgThrTrpGlyLeuArgValLeuasnArgLeuPheProSerSer 100  
 Db 389 ----- 389

Qy 101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116  
 Db 388 CAGAGAAGGAGTCGAGAACGCCAACGGCAAGCTGAAGCCCGAGCTC 340

RESULT 6

BX093784 LOCUS BX093784 Soares\_total\_fetus\_Nb2HF8\_9W Homo sapiens cDNA clone  
 DEFINITION BX093784 Soares\_total\_fetus\_Nb2HF8\_9W Homo sapiens cDNA clone  
 IMAGP9900B094758 ; IMAGE:1938800, mRNA sequence.  
 ACCESSION BX093784  
 VERSION BX093784.1 GI:27841729  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Ebert,L., Heil,O., Henning,S., Neubert,P., Partsch,E., Peters,M.,  
 Radefof,U., Schneider,D., and Korn,B.  
 TITLE Human Unigeneset - RZPD3  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Ina Rolfs  
 RZPD Deutsches RessourcenZentrum fuer Genomforschung GmbH  
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
 RZPD; IMAGP998E094758.  
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;  
 Human UniGeneset - RZPD; RZPD LIB No.372  
 http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response2libNo-972 Contact: Ina Rolfs  
 RZPD Deutsches RessourcenZentrum fuer Genomforschung GmbH  
 Heubnerweg 6, D-14059 Berlin, Germany  
 Tel: +49 30 32639 101  
 Fax: +49 30 32639 111  
 www.rzpd.de  
 This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:  
 M13r, Primer sequence: TTCACACGGAAACAGCTATGAC.

FEATURES  
 source 1. .478  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_Xref="taxon:9606"  
 /clone="IMAGE:998E094758" ; IMAGE:1938800"  
 /dev\_stage="8-9 weeks"  
 /lab\_host="DNI0B"  
 /clone\_lab="Soares total\_fetus\_Nb2HF8\_9w"  
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5'-TGTTACCAATTCTGAAGTGGAGGGCTTAATTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3D vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Alignment Scores:  
 Pred. No.: 3.63e-11 Length: 478  
 Score: 208.50 Matches: 50  
 Percent Similarity: 43.59% Conservative: 1  
 Best Local Similarity: 42.74% Mismatches: 0  
 Query Match: 33.85% Indels: 66  
 DB: 5 Gaps: 1  
 US-10-659-782A-32 (1-116) x BX093784 (1-478)

QY 1 MetProSerProGlyThrAlaCysSerIleLeuIleGlyMetLeuTerLeuAspIeu 20  
 Db 33 ATGCCCTCCCAGGACCCTCGAGCTCCGGCTGCTGGCTGGACTTG 92  
 QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40  
 Db 93 GCCATGGCAGGCTCCAGCTCCCTGAAACCCAGAGCTC----- 137  
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCyBAspLeuGlu 60  
 Db 137 ----- 137  
 QY 61 GluGlnArgHistTrpAlaSerValPheSerGlnSerThrLysAspSerAspLeu 80  
 Db 137 ----- 137  
 QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100  
 Db 137 ----- 137  
 QY 101 Arg-GluArgSerArgGlySerHisGlnProSerCysSerProGluLeu 116  
 Db 138 CAGAGAAGGAGTCGAGAAGGCCAACGCTGAGCCCCGAGCTC 186

RESULT 7  
 AY413164  
 LOCUS YAY413164  
 DEFINITION Pan troglodytes HCM4799 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
 ACCESSION AY413164  
 VERSION GSS  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE Clark A.G., Golanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanebaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,

Adams M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios Science 302 (5652), 1960-1963 (2003)  
 Adams M.D. and Cargill,M. Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 This sequence was made by sequencing genomic exons and ordering the sequence based on alignment.  
 Location/Qualifiers  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 <1..>334  
 /locus\_tag="HCM4799"

TITLE Adams M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 JOURNAL 14671302  
 PUBLMED 2 (bases 1 to 334)  
 AUTHORS Clark, A.G., Golanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanebaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams, M.D. and Cargill, M.  
 TITLE Adams M.D. and Cargill, M.  
 JOURNAL Direct Submission  
 COMMENT Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 FEATURES This sequence was made by sequencing genomic exons and ordering the sequence based on alignment.  
 source  
 gene  
 ORIGIN

Alignment Scores:  
 Pred. No.: 3.19e-11 Length: 334  
 Score: 207.00 Matches: 50  
 Percent Similarity: 43.59% Conservative: 1  
 Best Local Similarity: 42.74% Mismatches: 1  
 Query Match: 33.60% Indels: 65  
 DB: 9 Gaps: 1  
 US-10-659-782A-32 (1-116) x AY413164 (1-334)

QY 1 MetProSerProGlyThrAlaCysSerIleLeuIleGlyMetLeuTerLeuAspIeu 20  
 Db 1 ATGCCCTCCCAGGACCCTCGAGCTCCGGCTGCTGGCTGGACTTG 60  
 QY 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40  
 Db 61 GCCTGGCAGGCTCAGCTCTGAGCCCTGAAACCCAGAGCTCCAG----- 108  
 QY 41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCyBAspLeuGlu 60  
 Db 108 ----- 108  
 QY 61 GluGlnArgHistTrpAlaSerValPheSerGlnSerThrLysAspSerAspLeu 80  
 Db 108 ----- 108  
 QY 81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100  
 Db 108 ----- 108  
 QY 101 Arg-GluArgSerArgGlySerHisGlnProSerCysSerProGluLeu 116  
 Db 109 CAGAGAAGGAGTCGAGAAGGCCAACGCTGAGCCCCGAGCTC 157

RESULT 8  
 CE845760/c  
 LOCUS tigr\_gss-dog-17000332741330  
 DEFINITION GSS 01-OCT-2003  
 ACCESSION CE845760  
 VERSION CE845760.1  
 KEYWORDS GSS  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 REFERENCE Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 AUTHORS Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and

JOURNAL	Venter, J.J.	COMMENT	The dog genome: survey sequencing and comparative analysis
MEDLINE	Science 301 (5641), 1898-1903 (2003)	PUBMED	14512627
DEFINITION	Contact: Kirkness EF The Institute for Genomic Research Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville MD 20850, USA Tel: 301-838-0200 Fax: 301-838-0208 Email: ekirkness@tigr.org	ACCESSION	BI007288
VERSION	1	KEYWORDS	REVIEW 9
ORGANISM	Homo sapiens (human)	SOURCE	BI007288
REFERENCE	1	AUTHORS	NIH-MGC 1 to 542
TITLE	NIH-MGC	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)		COMMENT	
Contact: Robert Strausberg, Ph.D.			
Email: cgabbs@mail.nih.gov			
Tissue Procurement: Life Technologies, Inc.			
cDNA Library Preparation: Life Technologies, Inc.			
DNA Sequencing by: Invitae Genomics, Inc.			
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://imgc.llnl.gov			
Plate: LIAM1534 row: d column: 17			
High quality sequence stop: 535.			
Location/Qualifiers		FEATURES	
source		source	
1. . 542		/organism="Homo sapiens"	
		/mol_type="mRNA"	
		/db_xref="taxon:9606"	
		/clone="IMAGE:5212788"	
		/tissue_type="leukocyte"	
		/lab_host="DH10B"	
		/note="Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."	
ORIGIN		Alignment Scores:	
		Pred. No. :	3.32e-09
		Score:	190.00
		Percent Similarity:	43.5%
		Best Local Similarity:	42.74%
		Query Match:	30.84%
		DB:	4
		US-10-659-782A-32 (1-116) x BI907288 (1-542)	
		Qy	1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTerPheAspLeu 20
		Db	40 ATGCCCTCCGGGAC-GTCAGCTCCGCTCCCTGCGCATGCTCTGACTTG 98
		Qy	21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40
		Db	99 GCATGGAGGTCAAGCTCTGAGCTCTGACACCAGAGTCCTGAGCTCCAG 146
		Qy	41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLeuCysAspLeuGlu 60
		Db	146 -----
		Qy	61 GluGlnArgHistTrpAlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeu 80
		Db	146 -----
		Qy	81 ThrValSerGlyArgThrTrpGlyLeuArgValLeuAsnArgLeuPheProProSerSer 100
		Db	146 -----
FEATURES		RESULT 10	
Source		AA53094/C	
1. . 542		LOCUS	AA53094
		DEFINITION	nj01a01.s1 NCI_CGAP_Pr22 Homo sapiens mRNA sequence.
		ACCESSION	101 Arg-GluArgSerArgArgSerHisGlnProSerCysSerProGluLeu 116
		VERSION	147 CAGAAAGGAGTCGAAGCCACCCAACTGGCCGGCTC 195
		KEYWORDS	
		SOURCE	
		ORGANISM	
		REFERENCE	
		AUTHORS	
		TITLE	

KEYWORDS	EST.	Qy	104 SerArgArgSerHisGlnProSerCysSerProGluLeu 116
ORGANISM	Homo sapiens (human)	Db	376 AGTCGAGAAGGCCACCGCCAAAGCTGCAGCCCCGAGCTC 338
REFERENCE	1 (bases 1 to 600)	LOCUS	BY708559 523 bp mRNA linear EST 16-DEC-2002
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	DEFINITION	RIKEN full-length enriched, adult male stomach Mus musculus cDNA clone 2210006E23 5', mRNA sequence.
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	RESULT	BY708559
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	VERSION	BY708559.1 GI:27119750
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: rgs@MAIL.nih.gov	SOURCE	Mus musculus (house mouse)
FEATURES	<p>Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.</p> <p>cDNA Library Preparation: M. Bento Soares, Ph.D.</p> <p>cDNA Library Arrayed by: Greg Lennon, Ph.D.</p> <p>DNA Sequencing by: Washington University Genome Sequencing Center</p> <p>Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNLL at: www-bio.Ilnl.gov/bbrrp/image/image.html</p> <p>Insert Length: 1417 Std Error: 0.00</p> <p>Seq primer: -40m13 fwd. ET from Amersham</p> <p>High quality sequence stop: 314.</p> <p>Location/Qualifiers</p> <ul style="list-style-type: none"> <li>1..600</li> <li>/organism="Homo sapiens"</li> <li>/mol_type="mRNA"</li> <li>/db_xref="taxon:9606"</li> <li>/clone="IMAGE:9856608"</li> <li>/sex="male"</li> <li>/tissue_type="normal prostate"</li> <li>/lab_host="DH110B"</li> <li>/clone_id="NCI CGAP Pr22"</li> </ul> <p>/notes="Organ: prostate; vector: pRT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."</p>	ORGANISM	Mus musculus
ORIGIN		REFERENCE	1 (bases 1 to 523)
PREDICTED		AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamamoto, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Built, C., Hume, D.A., Quackenbush, J., Schizimi, L.M., Kanspini, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brodt, D., Brusic, V., Chotila, C., Corbani, J.B., Cousins, E., Dalla, F., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garibaldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawabaya, Y., Kedzierski, R.M., King, B.L., Kongaya, A., Kurochkin, I.V., Lee, Y., Lenhoff, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, J., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J.J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takehara, Y., Taylor, M.S., Tewdale, R.D., Tomita, M., Verardo, R., Wahlestedt, C., Wang, Y., Watanebe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayashi, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, X., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imamura, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
ALIGNMENT		TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
SCORE		JOURNAL	Nature 420, 563-573 (2002)
COMMENT		COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp URL: http://genome.gsc.riken.jp/
DBLINK		ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., CARNINCI, P., FUKUDA, S., HASHIZUME, W., HAYASHIZAKI, K., HIROZANE, T., HORI, F., IMOTONI, K., ISHII, Y., ITOH, M., KAGIWA, I., KAWAI, J., KOJIMA, Y., KONDO, S., KONNO, H., KOYA, S., MIYAZAKI, A., MURATA, M., NAKAMURA, M., NOMURA, K., NUMAZAKI, R., OHNO, M., OHSATO, N., SAITO, R., SAKAZUME, N., SINO, H., SAKAI, D., STO, K., SHIBATA, K., SHIRAKI, T., TAGAMI, M., TAKEDA, Y., WAKI, K., WATANAKI, A., MURAMATSU, M. and HAYASHIZAKI, Y.	
DIRECT		Direct Submission	Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
SUBMISSION			Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
REMARKS			RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11(2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

#### Location/Qualifiers

1. .323  
 /organism="Mus musculus"  
 /mol type="mRNA"  
 /db\_xref="Taxon:10050"  
 /sex="male"  
 /tissue\_type="stomach"  
 /dev\_stage="adult"  
 /clone\_lib="RIKEN full-length enriched, adult male stomach"  
 /note="Site 1: XhoI; Site 2: SstI; cDNA 1 library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGACGGCCAACTCGAGTTCCTTTTNTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCCTCGAATTAATTATTCCCCCCCCC 3']. cDNA was cleaved with Xhol and SstI."

#### ORIGIN

#### Alignment Scores:

Pred. No.: 5.3e-08 Length: 523  
 Score: 178.00 Matches: 54  
 Percent Similarity: 45.71% Conservative: 10  
 Best Local Similarity: 38.57% Mismatches: 39  
 Query Match: 28.90% Indels: 37  
 DB: 6 Gaps: 5

US-10-659-782A-32 (1-116) × BY708559 (1-523)

Qy 1 MetProSerProGlyThrValCysSerLeuLeuLeuGlyMetLeuTripleAspLeu 20  
 Db . 40 ATCGCTTTCAGCACATCSCAGTTGCTACTCAGATGTCTGGATGATG 99  
 Qy 21 AlaMetAlaGlySerSerPheLeuSerProGluHisGlnArgValGlnValArgProPro 40  
 Db 100 GCCATGGGCTCCAGCTTCCAGCCAGACACAGAAAGCCAGAGAA 159  
 Qy 41 HisLysAlaProGlnValProAlaLeuProLeuSerArgClnLeuCysBspIgLu 60  
 Db 160 TCCAGAACCCA-----CCGCTAACTGCGGCCAGACGAGCTCTGCAA 201  
 Qy 61 GlnglnAqghis----- 64  
 Db 202 GGCTGGCTCACCAAGGAGACAGGAGAACAGGAGAACAGAGGAGCTGGAGATC 261  
 Qy 65 ---TTPAlaSerValPheserGinSerThrLysAspSerGlySerAspLeuThrValser 83  
 Db 262 AGGTCAATGCTCCCTGATGTTGGCTCAAGCTGTAGGAGCTCATATAGCAGCAT 321  
 Qy 84 GlyArgThr-TrgGlyLeuArgValLeuAsnArgLeuPheProProSerSerArgGluAr 103  
 Db 322 GGCGGGCCCTGGGA-----AGTTCTCAGGATATCTCAGGAGAG 366  
 Qy 103 gSerArgArg-----SerHisGln-----ProSerCysSerPro 114

FEATURES	source	Db	367	:    GTCAAGGGGCCAGCTGACAAGTAACCGGAGAGGGCTGACCCGGTCTCT 424
		RESULT 12		
		AK008658	527 bp	mRNA linear
	LOCUS	AK008658	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210006B23 Product:GHRELIN PRECURSOR, full insert sequence.	
	DEFINITION	AK008658		
	KEYWORDS	AK008658_1	HTC; CAP trapper.	
	VERSION	GI:12842985		
	SOURCE	Mus musculus (house mouse)		
	ORGANISM			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
		Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning	1	
	REFERENCE			
	AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
	TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
	JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
	PUBMED	1042159		
	REFERENCE			
	AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, T., Fujiiwae, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Wakahiki, M., Yoneda, Y., Ishikawa, T., Ochiai, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.		
	TITLE	RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer		
	JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
	PUBMED	11076861		
	REFERENCE			
	AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.		
	TITLE	Functional annotation of a full-length mouse cDNA collection		
	JOURNAL	Nature 409, 685-690 (2001)		
	REFERENCE			
	AUTHORS	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
	TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
	JOURNAL	Nature 420, 563-573 (2002)		
	REFERENCE			
	AUTHORS	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Oho, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shiba, K., Shibata, Y., Shinagawa, A., Shirakawa, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, P., Tanaka, T., Teijima, Y., Toya, T., Yamamuro, T., Yasunishi, A., Yoshida, K., Yoshihino, M., Muramatsu, M., and Hayashizaki, Y.		
	TITLE	Direct Submission (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,		

COMMENT	URL: <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a> , Tel:81-45-503-9222, Fax:81-45-503-9156 Please visit our web site ( <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a> ) for further details.	Db	266 AGGTCAATGCTCCCTCGATTTGGCATCAAGCTCAGGACCTCAGTATCAGCAGCAT 325
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research contributed to preparation mouse tissues. First strand cDNA was primed with a primer [5', GAGAGAGAAGGATCCAAGAGCTCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trichloroethane activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAATTCCTCGATTTTAACTCCCCCCC 3'], cDNA was cleaved with XbaI and SstI. Cloning sites, 5' end: XbaI, 3' end: SstI.	Qy	84 GlyArgThr-TyrGlyLeuArgValLeuAsnArgLeuPheProProSerSerArgGluVar 103
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research contributed to preparation mouse tissues. First strand cDNA was primed with a primer [5', GAGAGAGAAGGATCCAAGAGCTCTCTTTTTTTTTTNN 3'], cDNA was prepared by using trichloroethane activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAATTCCTCGATTTTAACTCCCCCCC 3'], cDNA was cleaved with XbaI and SstI. Cloning sites, 5' end: XbaI, 3' end: SstI.	Db	326 GGCGGCCGCTGGGA-----AGTTCTCAGGATATCCTCTGGAAAGAG 370
		Qy	103 gSerArgArg-----SerHisGln-----ProSerCysserPro 114
		Db	371 GTCAAGAGGGCCAGCTGACAGTAGAACCGCACGGCTGCTGGCTTCCT 428
FEATURES	RESULT 13		
SOURCE	AK008860	LOCUS	AK008860 528 bp mRNA linear HTC 03-APR-2004
		DEFINITION	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210408M22 product:GHRELIN PRECURSOR, full insert sequence.
		ACCESSION	AK008860
		VERSION	AK008860.1 GI:12843305
		KEYWORDS	HTC; CAP trapper.
		SOURCE	Mus musculus (house mouse)
		ORGANISM	Mus musculus
CDS		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus .	
		REFERENCE 1	Carninci, P. and Hayashizaki, Y.
		AUTHORS	Carninci, P. and Hayashizaki, Y.
		JOURNAL	High-efficacy full-length cDNA cloning
		MEDLINE	Enzymol. 303, 19-44 (1999)
		PUBMED	99275253
		REFERENCE 2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
		AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
		JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
		MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)
		PUBMED	11042159
		REFERENCE 3	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishina, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
		AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishina, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
		JOURNAL	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
		MEDLINE	Genome Res. 10 (11), 1757-1771 (2000)
		PUBMED	2049374
		REFERENCE 4	The RIKEN Genome Exploration Research Group Phase II team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
		AUTHORS	Nature 409, 685-690 (2001)
		JOURNAL	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
		MEDLINE	Nature 420, 563-573 (2002)
		PUBMED	20530913
		REFERENCE 5	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
		AUTHORS	Nature 420, 563-573 (2002)
		JOURNAL	6 (bases 1 to 528)
		MEDLINE	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirota, T., Hori, F., Imocani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Koijima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibusawa, K., Shibusawa, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
		PUBMED	11076861
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		Best Local Similarity: 45.71%	Conservatives: 10
		Query Match: 38.57%	Mismatches: 39
		DB: 104	Indels: 37
		Gap: 3	Gap: 5
Qy	1 MetProSerProGlyThrValCysSerIleLeuLeuGlyMetLeuIleAspIeu 20	ALIGNMENT	
Db	44 ATGCTGTTCTGAGCACCATTCTGAGTTGCTGTGCTGACTAGCATGCTCTGGATGACTG 103	ALIGNMENT	
Qy	21 AlanylAlaGlySerSerPhelSerProGluLysGlnArgValGlnValArgProPro 40	ALIGNMENT	
Db	104 GCCATGGCAGGCTCCAGCTCTGAGCCAGAACGCCRCAGAACAGAA 163	ALIGNMENT	
Qy	41 HisLysAlaProHisValValProAlaLeuProLeuSerAsnGlnLysSer 60	ALIGNMENT	
Db	164 TCCAGAAACCA-----CCAGCTAACTGCAGGCCAGAACAGAA 205	ALIGNMENT	
Qy	61 GluGlnArgHis----- 64	ALIGNMENT	
Db	206 GGCTCGCTCCACCCAGGAAACAGGACAAGCAAGGACAGAGCTGGAGATC 265	ALIGNMENT	
Qy	65 ---TPAlaSerValpheserGlnSerThrLysAspSerGlySerAspLeuThrValser 83	ALIGNMENT	



US-10-659-782a-32 (1-116) x CK371838 (1-581)

Qy 3 SerProGlyThrValCysSerLeuLeuLeuLeuGlyMetLeuTrpLeuAspLeuAlaMet 22  
 Db 220 TCTTCAGGACCACTTGAGCTTCTGTACTCGATGCTCTGGATGACAGNGCCATG 279

Qy 23 AlaGlySerSerPheLeuSerProGluHisGlnArgValAlaArgProProHislys 42  
 Db 280 GCAGGCTCAGCTTCCTGAGGCCAGGACCCAGAGAAAGGATCCAG 339

Qy 43 AlaProHisValValProLeuProLeuSerAsnGlnLeuCysASLLeuGluGlnGln 62  
 Db 340 AAGCCA-----CCAGCTAACTGCACCGAGCTCTGGAGGCCAGCTGG 381

Qy 63 ArgHis-----Trp 65  
 Db 382 CTCCACCAGAGGACAGGAGACAAGGAGAGAGAGAGAGAGAGCTGGAGATCAGGTTC 441

Qy 66 AlaSerValPheSerGlnSerThrLysAspSerGlySerAspLeuThrValSerGlyArg 85  
 Db 442 AACCTCCCTTCAGTGTGGCATTAAGCTGTCAGGCTCAGTCATGGCATGGCC 501

Qy 86 Thr-TrpGlyLeuArgValLeuAsnArgLeupheProProSerSerArgGluArgSerArg 105  
 Db 502 GCCCTGGCA-----AGTTCTCAGGATAATCCTCTGGAAAGGGTCAA 546

Qy 105 GArg 106  
 Db 547 GAGG 550

RESULT 15  
 CF424809  
 LOCUS CF424809 587 bp mRNA linear EST 03-SEP-2003  
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 similar to TR:Q9YH7|Q9YH7|GRELIN PRECURSOR.; mRNA sequence.  
 ACCESSION CF424809  
 VERSION GI:34437510  
 KEYWORDS EST  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 587)  
 AUTHORS Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J.,  
 Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,  
 Ronko,I., Tsagareishvili,R., Belaygorod,L., Graw,R., Maguire,L.,  
 Waterston,R., and Wilson,R.

TITLE Unpublished (2002)

JOURNAL COMMENT Contact: Jeff Gordon and Mike Lovett  
 washU, Human Genetics Division

COMMENT Washington University School of Medicine  
 1st strand of cDNA was synthesized with reverse transcriptase and  
 oligo(dT) beads, then cDNA was amplified by PCR using modified  
 SMART Primers. The final cDNA was cloned in pAMP1 vector in  
 annealing reaction with Uracil DNA Glycosylase (UDG). Library  
 constructed by Y.Korshunova and M. Lovett. Library materials  
 provided by Mills JC & Gordon JI.

FEATURES Seq Primer: -40RP from Gibco.  
 source Location/Qualifiers  
 1. \*587  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
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 /dev\_stage="adult"  
 /clone\_lib="Gastric Epithelial Progenitor"  
 /lab\_host="DH5alpha"  
 /note=Vector: pAMP1; This library was created from  
 laser-captured isthmus cells from tox176 transgenic mice.  
 1st strand of cDNA was synthesized with reverse  
 transcriptase and oligo(dT) beads, then cDNA was amplified  
 by PCR using modified SMART primers. The final cDNA was

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